

(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 1 174 509 A1

(12)

EUROPEAN PATENT APPLICATION
published in accordance with Art. 158(3) EPC

(43) Date of publication:
23.01.2002 Bulletin 2002/04

(51) Int Cl.⁷: **C12N 15/55**, C12N 5/10,
C12P 21/08, C07K 16/40

(21) Application number: **00911431.5**

(86) International application number:
PCT/JP00/01918

(22) Date of filing: **28.03.2000**

(87) International publication number:
WO 00/58480 (05.10.2000 Gazette 2000/40)

(84) Designated Contracting States:
**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU
MC NL PT SE**
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **29.03.1999 JP 8719299**
24.06.1999 JP 17899999
27.12.1999 JP 37138299

(71) Applicants:
• **Kansai Technology Licensing Organization Co.,
Ltd.**
Kyoto-shi, Kyoto 600-8815 (JP)

• **Honjo, Tasuku**
Kyoto-shi, Kyoto 606-0001 (JP)

(72) Inventors:
• **HONJO, Tasuku**
Sakyo-ku, Kyoto-shi, Kyoto 606-0001 (JP)
• **MURAMATSU, Masamichi**
Sakyo-ku, Kyoto-shi, Kyoto 606-0954 (JP)

(74) Representative: **VOSSIUS & PARTNER**
Siebertstrasse 4
81675 München (DE)

(54) **NOVEL CYTIDINE DEAMINASE**

(57) Genes encoding novel proteins named AID (Activation-Induced cytidine Deaminase), having structural relationship to APOBEC-1, one of RNA editing enzymes, and having a cytidine deaminase activity similar to APOBEC-1, has been found by preparing cDNA

libraries for mouse B cell clone CH12F3-2, which undergoes class switch recombination from IgM to IgA at an extremely high rate together with activation of cells by stimulation with cytokines, with and without stimulating with cytokine, and performing subtraction cloning using the libraries.

EP 1 174 509 A1

DescriptionTechnical Field

[0001] The present invention relates to novel proteins having a cytidine deaminase activity; DNAs and fragments thereof (cDNAs, genomic DNAs, and primer DNAs) encoding the proteins; expression vectors comprising the DNAs; transformants transformed with the expression vectors; antibodies reactive to the proteins or fragments thereof; cells producing the antibodies; and methods for identifying substances that regulate production of the proteins, transcription of genes encoding the proteins into mRNAs, or enzyme activities of the proteins.

Background Art

[0002] The germinal center of mammals comprises a highly specialized microenvironment required for the final process of maturation towards antigen specific memory cells and long-lived plasma cells (Embo J., Vol.16, No.11, p. 2996-3006, 1999; Semin. Immunol., Vol.4, No.1, p.11-17, 1992). In the microenvironment, it is known that two fundamental editing of the immunoglobulin genes take place (J. Exp. Med., Vol.173, No.5, p.1165-1175, 1991; Embo. J., Vol.12, No.13, p.4955-4967, 1993; Adv. Exp. Med. Biol., Vol.186, p.145-151, 1985; Nature, Vol.342, No.6252, p. 929-931, 1989; Cell, Vol.67, No.6, p.1121-1129).

[0003] One is the somatic hypermutation (Curr. Opin. Immunol., Vol.7, No.2, p.248-254, 1995; Annu. Rev. Immunol., Vol.14, p.441-457, 1996; Science, Vol.244, No.4909, p.1152-1157, 1989), a phenomenon in which extensive point mutation of exon genes encoding variable regions of immunoglobulin occurs. Accumulation of the point mutation leads to selection of B cells expressing high affinity immunoglobulins on their cell surface, accompanied by the affinity maturation of antibodies (Embo. J., Vol.4, No.2, p.345-350, 1985; Proc. Natl. Acad. Sci. USA, Vol.85, No.21, p.8206-8210, 1988). As the result, immunoglobulin genes are edited as new functional genes.

[0004] Another is the class switch recombination (CSR). In the recombination, effector functions of antibodies, such as complement fixation, are selected by exchanging exons encoding constant region of immunoglobulin heavy chain (Curr. Top. Microbiol. Immunol., Vol.217, p.151-169, 1996; Annu. Rev. Immunol., Vol.8, p.717-735, 1990).

[0005] These two types of genetic editing are very important for effective humoral immunoreaction to eliminate harmful microbes. The molecular mechanisms of the genetic phenomena have not yet elucidated despite the extensive studies for several decades.

[0006] The present inventors isolated mouse B cell clone, CH12F3-2, as a research tool to elucidate the molecular mechanism of class switch recombination of immunoglobulin. In the B cell line, class switch recombination (CSR) from IgM to IgA begins several hours after stimulation with IL-4, TGF- β , and CD40L, and finally, over 80% of the cells become IgA positive (Immunity, Vol.9, p.1-10, 1998; Curr. Biol., Vol.8, No.4, p.227-230, 1998; Int. Immunol., Vol.8, No.2, p. 193-201, 1996).

[0007] Using the mouse B cell clone CH12F3-2, the present inventors had reported that the breakpoints of CSR distribute not only in switch region (S region), characteristic repeated sequences, but also in the neighboring sequences (Curr. Biol., Vol.8, No.4, p.227-230, 1998). However, the breakpoints were rarely seen in I exon and C exon, locating at upstream and downstream of S region, respectively. Also, according to the accumulated scientific evidence, it has been shown that the transcription of I exon and C exon and the splicing of the transcripts are essential for CSR (Cell, Vol.73, No.6, p. 1155-1264, 1993; Science, Vol.259, No.5097, p.984-987, 1993; Proc. Natl. Acad. Sci. USA, Vol.90, No.8, p.3705-3709, 1993; Cell, Vol.81, No.6, p.833-836, 1995).

[0008] This namely suggests that the transcripts are involved in CSR either directly or indirectly. Accordingly, the present inventors propose a theory that class switch is initiated by the recognition of DNA-RNA complex structure and not by the recognition of nucleotide sequences of switch region. This idea is further fortified by the fact that even in the case that S α region is substituted with S ϵ region or S γ region by introducing a mini-chromosome to above-mentioned mouse B cell clone CH12F3-2, CSR in the mini-chromosome efficiently occurs by stimuli of cytokines (Immunity, Vol. 9, p.1-10, 1998).

[0009] In plants and Protozoa, RNA editing, another type of genetic editing, is widely used as a mean for producing functional genes from limited genome (Cell, Vol.81, No.6, p.833-836, 1995; Cell, Vol.81, No.6, p.837-840, 1995). mRNA editing of many molecules such as mRNA of apolipoprotein B (apoB), AMPA receptors, Wilmstumor-1, α -galactosidase and neurofibromatosis type-1, and tRNA-Asp, have been reported (Trends Genet., Vol.12, No.10, p.418-424, 1996; Curr. Opin. Genet. Dev., Vol.6, No.2, p.221-231, 1996). Although the molecular mechanism of mammalian RNA editing has not yet been elucidated, one performed by APOBEC-1 (apolipoprotein B mRNA editing enzyme, catalytic polypeptide-1) becomes understood by degrees (Science, Vol.260, No.5115, p.1816-1819, 1993; J. Biol. Chem., Vol.268, No. 28, p.20709-20712, 1993).

[0010] In apoB RNA editing, the first base C (cytosine) of codon CAA, which encodes glutamine, is converted to U (uridine), which alters the codon to UAA. As the result, in-frame stop codon is made in the apoB mRNA (J. Cell., Vol.

81, No.2, p.187-195, 1995; J. Cell., Vol.50, No.6, p.831-840, 1987; Science, Vol.238, No.4825, p.363-266, 1987). apoB-48 and apoB-100 are transcripts of edited mRNA and unedited mRNA of apoB, respectively, and these proteins possess totally different physiological functions for each other (J. Biol. Chem., Vol.271, No.5, p.2353-2356, 1996).

[0011] In the site-specific RNA-editing, auxiliary factors are required (Science, Vol.260, No.5115, p.1816-1819, 1993; J. Biol. Chem., Vol.268, No.28, p.20709-20712, 1993). In the absence of auxiliary factors, APOBEC-1 shows only a cytidine deaminase activity, possessing non-specific low affinity to RNA (J. Biol. Chem., Vol.268, No.28, p.20709-20712, 1993; J. Cell., Vol.81, No.2, p.187-195, 1995; J. Biol. Chem., Vol.270, No.24, p.14768-14775, 1995; J. Biol. Chem., Vol.270, No.24, p.14762-14767, 1995). The expression and activity of the auxiliary factors are found not only in organs with apoB mRNA editing, but also in organs with undetectable level of APOBEC-1 expression, or organs without apoB mRNA editing (Science, Vol.260, No.5115, p.1816-1819, 1993; J. Biol. Chem., Vol.268, No.28, p.20709-20712, 1993; Nucleic Acids Res., Vol.22, No.10, p.1874-1879, 1994; Proc Natl. Acad. Sci. USA, Vol.91, No.18, p.8522-8526, 1994; J. Biol. Chem., Vol.269, No.34, p.21725-21734, 1994).

[0012] The unexpected expression of the auxiliary factors involved in apoB mRNA editing suggests that the auxiliary factors may be involved in more general cellular function or other yet unknown RNA editing. Since there are possibilities that CSR and hypermutation, which are genetic editing relating to immunoglobulin, may be accomplished by RNA editing, it is very interesting to elucidate whether RNA editing takes place or not in the genetic editing of immunoglobulin gene mentioned above.

Disclosure of the Invention

[0013] The present invention provides AID (Activation-Induced cytidine Deaminase), a novel cytidine deaminase having structural relationship to APOBEC-1, one of RNA editing enzyme, and involved in RNA editing in germinal center B cells, where genetic editing of immunoglobulin gene occurs, and a DNA encoding the enzyme.

[0014] The present inventors intensively searched for novel genes involved in class switch recombination (CSR), one of major genetic editing of immunoglobulin gene. As a result, by preparing cDNA libraries for mouse B cell clone CH12F3-2, in which class switch recombination from IgM to IgA is shown to occur at an extremely high rate together with activation of cells by stimulation with cytokines, with and without stimulating with cytokine, and performing subtraction cloning using the libraries, the present inventors found genes encoding mouse- and human-derived novel proteins named AID (Activation-Induced cytidine Deaminase), having structural relationship to APOBEC-1, one of RNA editing enzymes, and having a cytidine deaminase activity similar to APOBEC-1.

[0015] The AID protein in the present invention possesses features described below, and considered to be a very important RNA-modifying deaminase involved in regulating B cell activation, CSR of immunoglobulin gene, somatic hypermutation, and affinity maturation, which all are genetic editing specific to germinal center function:

(1) ORF of cDNA encoding AID protein comprises 198 amino acids, with 24kDa calculated molecular weight (mouse: SEQ ID NO: 2, and human: SEQ ID NO: 8). Mouse AID protein shows approximately 28kDa molecular weight by SDS-PAGE.

(2) The amino acid sequence of AID protein is 34% and 26% identical to APOBEC-1 (apolipoprotein B mRNA editing enzyme, catalytic polypeptide-1) at amino acid sequence level, for mouse and human derived protein respectively.

(3) AID protein has cytidine/deoxycytidine deaminase motif, which is the active center of the deaminase activity conserved in amino acid sequences of proteins belonging to cytosine nucleoside/nucleotide deaminase family.

(4) Cytidine deaminase motif of AID protein is allied with RNA editing deaminase subgroup.

(5) AID protein has Leucine-rich region considered to be important in protein-protein interaction, similar to APOBEC-1. Four leucines in leucine-rich region of the AID protein are conserved in leucine-rich region of APOBEC-1 in rabbit, rat, mouse and human.

(6) In the primary structure of AID protein, all amino acid residues reported to be necessary for APOBEC-1 to bind RNA (Phe66, Phe87, His61, Glu63 and Cys93) are conserved.

(7) AID protein has pseudoactive site domain in its C terminal for forming homodimer, similar to APOBEC-1 and ECDDA, an E. coli derived cytidine deaminase. There are possibilities that AID protein forms homodimer, or associates with other auxiliary proteins.

(8) AID protein shows a concentration-dependent cytidine deaminase activity. The activity can be inhibited dose dependently by tetrahydrouridine (THU), a specific inhibitor of cytidine deaminase. Also, a zinc chelator, 1,10-o-phenanthroline, inhibits the cytidine deaminase activity of AID protein while 1,7-o-phenanthroline, the inactive isomer, shows a weak inhibition. Thus, AID protein can be considered to be a zinc-dependent cytidine deaminase as APOBEC-1.

(9) Strong expression of AID mRNA expression is seen in lymph nodes (mesenteric and amygdaline). Also, weak expression in spleen is seen.

(10) mRNA expression of AID protein is seen in a variety of lymphoid tissues (Peyer's patch, mesenteric lymph node, axillary lymph node, spleen, and bone marrow). Especially, notable expression is seen in peripheral lymphoid organs, such as lymphatic nodes and Peyer's patch. Contrariwise, expression in primary lymphoid organs is lower than the peripheral lymphoid organs.

(11) Expression of AID mRNA is at detection limit level without cytokines (IL-4, CD40L, TGF- β) stimulation in mouse B cell clone CH12F3-2, in which the cytokines stimulate class switch from IgM to IgA in the cells, whereas the expression is induced 3 hours after stimulation, and maximal expression is seen after 12 hours, with cytokine stimulation.

(12) AID mRNA expression in mouse B cell clone CH12F3-2 can be induced strongly when stimulated with three cytokines, IL-4, CD40L and TGF- β , simultaneously, rather than stimulated with any one of them. Also, it can be considered that de novo protein synthesis is necessary for augmentation of AID mRNA expression, as the AID mRNA expression induction by cytokines in mouse B cell clone CH12F3-2 can be inhibited by cycloheximide, an protein synthesis inhibitor.

(13) In the in vitro test, an augmentation of AID mRNA expression can be seen when normal mouse spleen B cells are stimulated with LPS alone, LPS+IL-4, or LPS+TGF- β .

(14) In the in vivo test, when normal mice are immunized with sheep red blood cells (SRBC), a significant augmentation of AID mRNA expression can be seen 5days after immunization, in which SRBC are known to induce clonal expansion, germinal center formation, and class switch recombination and affinity maturation of immunoglobulin gene.

(15) The in vivo augmentation of AID mRNA expression by SRBC immunization is specifically seen in splenic CD19 positive B cells.

(16) AID mRNA expression in lymphoid organs is specifically seen in the germinal center, enriched with B cells activated by antigen stimulation.

(17) Human AID gene locates at locus 12p13, close to the locus 12p13.1, where APOBEC-1 gene locates.

[0016] According to the characteristics described above, the AID protein of the present invention can be considered to have a function of regulating various biological mechanisms required for generation of antigen-specific immunoglobulins (specific antibodies), which eliminate non-self antigen (foreign antigen, self-reacting cells, etc.) that triggers various diseases. The mechanism for generation of immunoglobulin having high specificity to antigens includes germinal center functions such as activation of B cells, class switch recombination of immunoglobulin gene, somatic hypermutation, and affinity maturation. The AID protein of the present invention can be considered to be one of the enzymes that play an important role in the genetic editing occurring in germinal center B cells (e.g. class switch recombination and somatic mutation).

[0017] The dysfunction of the AID protein of the present invention can be the cause for the humoral immunodeficiency since it induces failure of germinal center B cell function, such as antigen-specific B cell activation, class switch recombination, and somatic mutation. Reversely, the hyperfunction of AID protein may induce allergy disease or autoimmune disease since it can cause inappropriate B cell activation and needless class switch recombination and somatic mutation.

[0018] Therefore, regulation of the function of AID protein and the gene encoding it enables preventing and treating various immunodeficiencies, autoimmune diseases, and allergies, which result from, for example, B cell dysfunctions (e.g. IgA deficiency, IgA nephropathy, γ globulinemia, hyper IgM syndrome, etc.) or class switch deficiency of immunoglobulin. Thus, the AID protein and the gene encoding the AID protein can be targets for the development of drugs for therapy of diseases mentioned above.

[0019] Examples of diseases whose onset prevention, symptom remission, therapy and/or symptomatic treatment effect is expected by regulating the function of the AID protein of the present invention or the gene encoding it include, for example, primary immunodeficiency syndrome with congenital disorder of immune system, mainly various immunodeficiencies considered to develop by B cell deficiency, decrease, or dysfunction (e.g., sex-linked agammaglobulinemia, sex-linked agammaglobulinemia with growth hormone deficiency, immunoglobulin deficiency with high IgM level, selective IgM deficiency, selective IgE deficiency, immunoglobulin heavy chain gene deletion, κ chain deficiency, IgA deficiency, IgG subclass selective deficiency, CVID (common variable immunodeficiency), infantile transient dysgammaglobulinemia, Rosen syndrome, severe combined immunodeficiency (sex-linked, autosomal recessive), ADA (adenosine deaminase) deficiency, PNP (purine nucleoside phosphorylase) deficiency, MHC class II deficiency, reticular dysplasia, Wiskott-Aldrich syndrome, ataxia telangiectasia, DiGeorge syndrome, chromosomal aberration, familial Ig hypermetabolism, hyper IgE syndrome, Gitlin syndrome, Nezelof syndrome, Good syndrome, osteodystrophy, transcobalamin syndrome, secretory bead syndrome, etc.), various diseases with antibody production deficiency that are secondary immunodeficiency syndrome with disorder of immune system caused by an acquired etiology (for example, AIDS, etc.), and/or various allergic diseases (e.g., bronchial asthma, atopic dermatitis, conjunctivitis, allergic rhinitis, allergic enteritis, drug-induced allergy, food allergy, allergic urticaria, glomerulonephritis, etc.).

[0020] Namely, the AID protein of the present invention, a fragment thereof, a DNA encoding the AID protein, a fragment thereof, and an antibody against the AID protein are useful as reagents for developing drugs for prevention and therapy of such diseases.

[0021] Also, the DNA itself is useful as an antisense drug regulating the function of AID gene at a gene level and in a use in gene therapy. The protein or the fragments thereof (e.g. enzyme active site) itself is useful as a drug.

[0022] Furthermore, a DNA comprising a complementary nucleotide sequence to an arbitrary partial nucleotide sequence in the nucleotide sequence of genomic DNA encoding AID protein of the present invention (especially human AID protein) is useful as a primer DNA for polymerase chain reaction (PCR).

[0023] An arbitrary partial nucleotide sequence of genomic DNA encoding the AID protein (especially human AID protein) of the present invention can be amplified by PCR using the primer DNA pair. For example, in the case that mutation or deletion of the nucleotide sequence of genomic DNA (especially exon) encoding AID protein is presumed to cause a certain immunodeficiency or an allergy, mutations and deletions in the genomic DNA can be identified by amplifying an arbitrary partial nucleotide sequence of genomic DNA encoding the AID protein obtained from tissue or cells of immunodeficiency or allergy patients by PCR using a pair of the primer DNA, by analyzing the presence and the size of PCR products, and the nucleotide sequence of the PCR products, and by comparing the nucleotide sequence with the corresponding nucleotide sequence in the genomic DNA encoding the AID protein derived from the normal human. That is to say, this method is capable of not only, for example, elucidating relationships between immunodeficiency or allergy and AID protein, but also, in the case where AID protein is the cause of onset of a sort of disease (e.g. immunodeficiency and/or allergy), diagnosing the diseases by the methods mentioned above.

[0024] Furthermore, an antibody reactive to the AID protein of the present invention or a fragment thereof is extremely useful as an antibody drug by regulating functions of the AID protein.

[0025] Furthermore, the gene (DNA), protein, and antibody of the present invention are useful as reagents for searching substrates (e.g. RNA, etc.) interacting (binding) with the protein (enzyme) of the present invention, or other auxiliary proteins associated with the protein of the present invention, and for developing drugs targeting the substrates and auxiliary proteins.

[0026] Also, model animals can be generated by disrupting (inactivating) the AID gene base on the genetic information on the AID protein derived from mammals (e.g. mouse, etc.), which is one embodiment of the DNA of present invention. By analyzing the physical, biological, pathological, and genetic features of the model animal, it is possible to elucidate functions of the genes and the proteins of the present invention.

[0027] Furthermore, by introducing normal human AID gene or mutant human AID gene (e.g. mutant human AID genes derived from immunodeficiency patients), which is one embodiment of the present invention, into the model animal whose endogenous gene has been disrupted, model animals having only normal or mutant human AID genes of the present invention can be generated. By administering drugs (compounds, antibodies, etc.) targeting the introduced human AID genes to the model animals, therapeutic effects of the drugs can be evaluated.

[0028] Furthermore, a method for identifying a substance that regulates production of the AID protein of the present invention or transcription of a gene encoding the AID protein into mRNA, or a substrate that inhibits the enzyme activity of the AID protein (e.g. cytidine deaminase activity) are extremely useful as means to develop drugs for therapy and prevention of various diseases (especially, immunodeficiency and/or allergy) in which the above-mentioned AID protein or AID gene is considered to be involved.

[0029] Thus, the present invention, for the first time, provides blow-mentioned DNAs (cDNAs, genomic DNAs, and an arbitrary fragment thereof), proteins, expression vectors, transformants, antibody pharmaceutical compositions, cells, the use of the DNA fragments as primer DNAs, and methods for screening.

(1) A DNA or a fragment thereof encoding a protein comprising the amino acid sequence of SEQ ID NO: 2 or 8.

(2) The DNA or the fragment of (1), wherein the protein has a cytidine deaminase activity.

(3) A DNA or a fragment thereof comprising the nucleotide sequence of SEQ ID NO: 1 or 7.

(4) A DNA or a fragment thereof comprising a nucleotide sequence of (a) or (b) below:

(a) a nucleotide sequence comprising the nucleotide residues 93 to 689 of SEQ ID NO: 1 or

(b) a nucleotide sequence comprising the nucleotide residues 80 to 676 of SEQ ID NO: 7.

(5) A DNA or a fragment thereof of (a) or (b) below:

(a) a DNA or a fragment thereof that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1 and that encodes a mammal-derived protein being homologous to a protein that comprises the amino acid sequence of SEQ ID NO: 2 and having a cytidine deaminase activity or

(b) a DNA or a fragment thereof that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7 and that encodes a mammal-derived protein being homologous to a protein that

comprises the amino acid sequence of SEQ ID NO: 8 and having a cytidine deaminase activity.

(6) A protein or a fragment thereof comprising the amino acid sequence of SEQ ID NO: 2 or 8.

(7) A protein or a fragment thereof comprising substantially the same amino acid sequence as that of SEQ ID NO: 2 or 8 and having a cytidine deaminase activity.

(8) A proteins of (a) or (b) below.

(a) a mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 2, and that has a cytidine deaminase activity or
(b) a mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 8, and that has a cytidine deaminase activity.

(9) An expression vector comprising the DNA or the fragment of any one of (1) to (5).

(10) A transformant transformed with the expression vector of (9).

(11) An antibodies or a portion thereof reactive to the protein of any one of (6) to (8) or to a fragment of the protein.

(12) The antibodies or the portion of (11), wherein the antibody is a monoclonal antibody.

(13) A pharmaceutical composition comprising the antibody or the portion of (11) or (12), and a pharmaceutically acceptable carrier.

(14) A cell producing a monoclonal antibody reactive to the protein of any one of (6) to (8) or to a fragment of the protein.

(15) The cell of (14), wherein the cell is a hybridoma obtained by fusing, with a mammal-derived myeloma cell, a non-human mammal-derived B cell that produces a monoclonal antibody.

(16) The cell of (15), wherein the cell is a transgenic cell transformed by introducing, into a cell, either or both of a DNA encoding a heavy chain of the monoclonal antibody and a DNA encoding a light chain of the monoclonal antibody.

(17) A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (c) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10, or
- (c) SEQ ID NO: 35.

(18) A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (e) below:

- (a) SEQ ID NO: 11,
- (b) SEQ ID NO: 12,
- (c) SEQ ID NO: 13,
- (d) SEQ ID NO: 14, or
- (e) SEQ ID NO: 15.

(19) A DNA comprising a complementary nucleotide sequence to an arbitrary partial nucleotide sequence of a nucleotide sequence of any one of (a) to (h) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10,
- (c) SEQ ID NO: 11,
- (d) SEQ ID NO: 12,
- (e) SEQ ID NO: 13,
- (f) SEQ ID NO: 14,
- (g) SEQ ID NO: 15, or
- (h) SEQ ID NO: 25.

(20) The DNA of (19), wherein the DNA comprises a nucleotide sequence of any one of (a) to (q) below:

- (a) SEQ ID NO: 18,
- (b) SEQ ID NO: 19,
- (c) SEQ ID NO: 20,

- (d) SEQ ID NO: 21,
- (e) SEQ ID NO: 22,
- (f) SEQ ID NO: 23,
- (g) SEQ ID NO: 24,
- (h) SEQ ID NO: 25,
- (i) SEQ ID NO: 26,
- (j) SEQ ID NO: 27,
- (k) SEQ ID NO: 28,
- (l) SEQ ID NO: 29,
- (m) SEQ ID NO: 30,
- (n) SEQ ID NO: 31,
- (o) SEQ ID NO: 32,
- (p) SEQ ID NO: 33, or
- (q) SEQ ID NO: 34.

(21) Use of the DNA of (19) or (20) as a primer DNA in polymerase chain reaction.

(22) Use of a pair of DNA of any one of (a) to (n) below as primer DNAs in polymerase chain reaction:

- (a) a DNA comprising the nucleotide sequence of SEQ ID NO: 31 and a DNA comprising the nucleotide sequence of SEQ ID NO: 32,
- (b) a DNA comprising the nucleotide sequence of SEQ ID NO: 20 and a DNA comprising the nucleotide sequence of SEQ ID NO: 22,
- (c) a DNA comprising the nucleotide sequence of SEQ ID NO: 21 and a DNA comprising the nucleotide sequence of SEQ ID NO: 30,
- (d) a DNA comprising the nucleotide sequence of SEQ ID NO: 24 and a DNA comprising the nucleotide sequence of SEQ ID NO: 25,
- (e) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (f) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (g) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (h) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (i) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (j) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (k) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (l) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (m) a DNA comprising the nucleotide sequence of SEQ ID NO: 33 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29, or,
- (n) a DNA comprising the nucleotide sequence of SEQ ID NO: 18 and a DNA comprising the nucleotide sequence of SEQ ID NO: 19.

(23) A method for identifying a substance that regulates transcription of a gene encoding an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8 into mRNA, or production of the AID protein, the method comprising the steps of:

- (a) culturing, separately in the presence and the absence of the substance, cells producing the AID protein and
- (b) (i) comparing the level of the AID protein produced by the cells cultured in the presence of the substance with the level of the AID protein produced by the cells cultured in the absence of the substance or
- (ii) comparing the level of the AID protein-encoding mRNA transcribed in the cells cultured in the presence of the substance with the level of the AID protein-encoding mRNA transcribed in the cells cultured in the absence of the substance.

(24) A method for identifying a substance that regulates transcription of a gene encoding an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8 into mRNA, or production of the AID protein, the method comprising the steps of:

- (a) culturing, separately in the presence and the absence of the substance, cells producing the AID protein and a protein other than the AID protein, wherein transcription of a gene encoding the other protein into mRNA is dependent in the cells on the degree of a signal of transcription of the gene encoding the AID protein into mRNA and
- (b) comparing the level of the other protein produced by the cells cultured in the presence of the substance with the level of the other protein produced by the cells cultured in the absence of the substance.

(25) The method of (23) or (24), wherein the cells are transgenic cells transformed with a gene encoding the protein.

(26) The method of (24), wherein the cells are transgenic cells transformed with a gene encoding the protein and a gene encoding the other protein.

(27) The method of (26), wherein the protein is a reporter protein.

(28) The method of (27), wherein comparison of the level of the other protein is comparison of the level of a signal generated by the reporter protein.

(29) The method of (27) or (28), wherein the reporter protein is luciferase.

(30) A method for identifying a substance that inhibits an enzyme activity of an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8, the method comprising the step of (a) or (b) below:

- (a) culturing, separately in the presence and the absence of the substance, mammal-derived B cells or tissues comprising the B cells, and comparing enzyme activities of the AID protein in the B cells separately cultured or
- (b) (i) administering the substance separately to an AID gene knockout mouse whose endogenous AID gene is inactivated so that transcription of the endogenous AID gene into mRNA is inhibited, and to a normal mouse and
- (ii) comparing enzyme activities of the AID proteins in the B cells isolated from the respective mice.

(31) The method of (30), wherein the enzyme activity is a cytidine deaminase activity.

[0030] Hereafter, the present invention is explained in detail, by clarifying the terms used in the present invention and general methods for producing the proteins, DNAs, antibodies, and cells of the present invention.

[0031] The "protein or a fragment thereof" means a protein and a fragment thereof derived from a mammal such as human, bovine, sheep, pig, goat, rabbit, rat, hamster, guinea pig, mouse, and so on, preferably a protein or a fragment thereof derived from human, rabbit, rat, or mouse, and particularly preferably, a protein of a fragment thereof derived from human or mouse.

[0032] As a particularly preferred embodiment, it means any protein or a fragment thereof below.

(1) A protein or a fragment thereof comprising the amino acid sequence of SEQ ID NO: 2 or 8.

(2) A protein or a fragment thereof comprising substantially the same amino acid sequence as that of SEQ ID NO: 2 or 8 and having a cytidine deaminase activity.

(3) A mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 2, and that has a cytidine deaminase activity.

(4) A mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 8, and that has a cytidine deaminase activity.

[0033] Here, "having substantially the same amino acid sequence" means that a protein has an amino acid sequence where multiple amino acids, preferably 1 to 10 amino acids, particularly preferably 1 to 5 amino acids, in the amino acid sequence shown in the references are substituted, deleted, and/or modified, and that a protein has an amino acid sequence where multiple amino acids, preferably 1 to 10 amino acids, particularly preferably 1 to 5 amino acids, are added to the amino acid sequence shown in the references.

[0034] The protein of the present invention includes monomer molecule, homodimer in which one strand binds to another strand comprising an identical amino acid sequence, heterodimer in which one strand binds to another strand comprising a different amino acid sequence, and oligomers such as trimer or tetramer.

[0035] Also, the "fragment of a protein" means an arbitrary partial sequence (fragment) in the amino acid sequence that the above-mentioned AID protein of the present invention comprises. For example, it includes an enzyme active

site required for the AID protein to exert an enzyme activity represented by a cytidine deaminase activity, and an interaction site required for the AID protein to bind or associate with substrates (e.g. mRNA, etc.) or various auxiliary proteins.

[0036] Alphabetical triplet or single letter codes used to represent amino acids in the present specification or figures mean amino acids as follows:

[0037] (Gly/G), glycine; (Ala/A), alanine; (Val/V), valine; (Leu/L), leucine; (Ile/I), isoleucine; (Ser/S), serine; (Thr/T), threonine; (Asp/D), aspartic acid; (Glu/E), glutamic acid; (Asn/N), asparagines; (Gln/Q) glutamine; (Lys/K), lysine; (Arg/R), arginine; (Cys/C), cysteine; (Met/M), methionine; (Phe/F), phenylalanine; (Tyr/Y), tyrosine; (Trp/W), tryptophan; (His/H), histidine; (Pro/P), proline.

[0038] The proteins and fragments of the present invention can be produced by properly using, in addition to genetic engineering technique mentioned below, methods well known in the art, such as chemical synthesis, cell culture method, and so on, or their modified methods.

[0039] Also, the AID protein of the present invention can be produced as a recombinant fusion protein with other protein (e.g. GST (Glutathione S-transferase), etc.). In this case, the fusion protein is advantageous in that it can be extremely easily purified by affinity chromatography employing adsorbent on which other protein molecule binding specifically to GST is immobilized. Moreover, since various antibodies reactive to GST are provided, the quantification of the fusion protein can be simply carried out by immunoassay (e.g. ELISA, etc.) using the antibodies against GST.

[0040] The DNA of the present invention is a DNA encoding protein of the present invention and a fragment thereof, and it includes any nucleotide sequence encoding the protein of the present invention and includes both genomic DNAs and cDNAs. Also, the DNA includes any DNA composed of any codons as long as the codons encode identical amino acids.

[0041] Also, the DNA of the present invention includes a DNA encoding mammal AID protein, and, as a preferred embodiment, a DNA encoding mouse AID protein or human AID protein can be exemplified.

[0042] Examples of specific embodiments are as follows:

- (1) A DNA encoding a protein comprising the amino acid sequence of SEQ ID NO: 2 or 8.
- (2) The DNA of (1), wherein the protein has a cytidine deaminase activity.
- (3) A DNA comprising the nucleotide sequences of SEQ ID NO: 1 or 7.
- (4) A DNA comprising the nucleotide residues 93 to 689 of SEQ ID NO: 1.
- (5) A DNA comprising the nucleotide residues 80 to 676 of SEQ ID NO: 7.
- (6) A DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1 and that encodes a mammal-derived protein being homologous to a protein that comprises the amino acid sequence of SEQ ID NO: 2 and having a cytidine deaminase activity.
- (7) A DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7 and that encodes a mammal-derived protein being homologous to a protein that comprises the amino acid sequence of SEQ ID NO: 8 and having a cytidine deaminase activity.
- (8) A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (c) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10, or
- (c) SEQ ID NO: 35.

- (9) A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (e) below:

- (a) SEQ ID NO: 11,
- (b) SEQ ID NO: 12,
- (c) SEQ ID NO: 13,
- (d) SEQ ID NO: 14, or
- (e) SEQ ID NO: 15.

- (10) A DNA comprising a complementary nucleotide sequence to an arbitrary partial sequence of a nucleotide sequence of any one of (a) to (h) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10,
- (c) SEQ ID NO: 11,
- (d) SEQ ID NO: 12,
- (e) SEQ ID NO: 13,

- (f) SEQ ID NO: 14,
- (g) SEQ ID NO: 15, or
- (h) SEQ ID NO: 35.

5 (11) A DNA comprising a nucleotide sequence of any one of (a) to (q) below:

- (a) SEQ ID NO: 18,
- (b) SEQ ID NO: 19,
- (c) SEQ ID NO: 20,
- 10 (d) SEQ ID NO: 21,
- (e) SEQ ID NO: 22,
- (f) SEQ ID NO: 23,
- (g) SEQ ID NO: 24,
- (h) SEQ ID NO: 25,
- 15 (i) SEQ ID NO: 26,
- (j) SEQ ID NO: 27,
- (k) SEQ ID NO: 28,
- (l) SEQ ID NO: 29,
- (m) SEQ ID NO: 30,
- 20 (n) SEQ ID NO: 31,
- (o) SEQ ID NO: 32,
- (p) SEQ ID NO: 33, or,
- (q) SEQ ID NO: 34.

25 **[0043]** Furthermore, a DNA encoding a mutant protein or a fragment thereof obtained by substituting, deleting, and/or modifying multiple amino acids, preferably 1 to 10 amino acids, particularly preferably 1 to 5 amino acids, or by inserting multiple amino acids, preferably 1 to 10 amino acids, particularly preferably 1 to 5 amino acids in the amino acid sequence constituting the above-defined AID protein of the present invention or a fragment thereof is included in the DNA of the present invention.

30 **[0044]** The term "under stringent conditions" used herein means, for example, the following conditions. For example, in the case of carrying out hybridization using a probe with not less than 50 bases in 0.9% NaCl, target temperature of causing 50% dissociation (T_m) can be calculated from the formula below, and the hybridization temperature can be set as the formula below.

35
$$T_m = 82.3^{\circ}\text{C} + 0.41 \times (\text{G}+\text{C})\% - 500/n - 0.61 \times (\text{formamide})\% \quad (n \text{ means the number of bases of the probe})$$

Temperature = $T_m - 25^{\circ}\text{C}$

40 **[0045]** Also, in the case of using a probe with not less than 100 bases ($\text{G}+\text{C} = 40$ to 50%), the changes of T_m as (1) and (2) below can be used as the indicator.

- (1) Every 1% mismatch decreases T_m by approximately 1°C .
- (2) Every 1% formamide decreases T_m by 0.6 to 0.7°C .

45 **[0046]** Thus, the temperature condition in the case of combination of complete complementary strands can be set as below.

- (A) 65 to 75°C (without formamide)
- 50 (B) 35 to 45°C (with 50% formamide)

[0047] The temperature condition in the case of combination of incomplete complementary strands can be set as below.

- 55 (A) 45 to 55°C (without formamide)
- (B) 35 to 42°C (with 30% formamide)

[0048] In the case of using probes with not more than 23 bases, temperature can be 37°C , or the formula below can

also be used as an indicator.

$$\text{Temperature} = 2^{\circ}\text{C} \times (\text{number of A+T}) + 4^{\circ}\text{C} \times (\text{number of C+G}) - 5^{\circ}\text{C}$$

[0049] The DNA of the present invention can be a DNA obtained by any method. For example, the DNA includes complementary DNA (cDNA) prepared from mRNA, DNA prepared from genomic DNA, DNA prepared by chemical synthesis, DNA obtained by PCR amplification with RNA or DNA as a template, and DNA constructed by appropriately combining these methods.

[0050] The DNA encoding the protein of the present invention can be prepared by the usual methods: cloning cDNA from mRNA encoding the protein of the present invention, isolating genomic DNA and splicing it, chemical synthesis, and so on.

[0051] (1) cDNA can be cloned from mRNA encoding the protein of the present invention by, for example, the method described below.

[0052] First, the mRNA encoding the protein of the present invention is prepared from the above-mentioned tissues or cells expressing and producing the protein of the present invention. mRNA can be prepared by isolating total RNA by a known method such as guanidine-thiocyanate method (Chirgwin et al., Biochemistry, Vol.18, p.5294, 1979), hot phenol method, or AGPC method, and subjecting it to affinity chromatography using oligo-dT cellulose or poly-U Sepharose.

[0053] Then, with the mRNA obtained as a template, cDNA is synthesized, for example, by a well-known method using reverse transcriptase, such as the method of Okayama et al (Mol. Cell. Biol. Vol.2, p.161 (1982) ; Mol. Cell. Biol. Vol.3, p.280 (1983)) or the method of Hoffman et al. (Gene Vol.25, p.263 (1983)), and converted into double-stranded cDNA. A cDNA library is prepared by transforming *E. coli* with plasmid vectors, phage vectors, or cosmid vectors having this cDNA or by transfecting *E. coli* after in vitro packaging.

[0054] The plasmid vectors used in this invention are not limited as long as they are replicated and maintained in hosts. Any phage vector that can be replicated in hosts can also be used. Examples of usually used cloning vectors are pUC19, λ gt10, λ gt11, and so on. When the vector is applied to immunological screening as mentioned below, a vector having a promoter that can express a gene encoding the desired protein in a host is preferably used.

[0055] cDNA can be inserted into a plasmid by, for example, the method of Maniatis et al. (Molecular Cloning, A Laboratory Manual, second edition, Cold Spring Harbor Laboratory, p.1.53, 1989). cDNA can be inserted into a phage vector by, for example, the method of Hyunh et al. (DNA cloning, a practical approach, Vol.1, p.49 (1985)). These methods can be simply performed by using a commercially available cloning kit (for example, a product from Takara Shuzo). The recombinant plasmid or phage vector thus obtained is introduced into an appropriate host cell such as a prokaryote (for example, *E. coli*: HB101, DH5 α , MC1061/P3, etc).

[0056] Examples of a method for introducing a plasmid into a host are, calcium chloride method, calcium chloride/rubidium chloride method and electroporation method, described in Molecular Cloning, A Laboratory Manual (second edition, Cold Spring Harbor Laboratory, p.1.74 (1989)). Phage vectors can be introduced into host cells by, for example, a method in which the phage DNAs are introduced into grown hosts after in vitro packaging. In vitro packaging can be easily performed with a commercially available *in vitro* packaging kit (for example, a product from Stratagene or Amersham).

[0057] The identification of cDNA encoding protein, its expression being augmented depending on the stimulation of cytokines like AID protein of the present invention, can be carried out by for example suppression subtract hybridization (SSH) (Proc. Natl. Acad. Sci. USA, Vol.93, p.6025-6030, 1996; Anal. Biochem., Vol.240, p.90-97, 1996) taking advantage of suppressive PCR effect (Nucleic Acids Res., Vol.23, p.1087-1088, 1995), using two cDNA libraries, namely, cDNA library constructed from mRNA derived from stimulated cells (tester cDNA library) and that constructed from mRNA derived from unstimulated cells (driver cDNA library).

[0058] The preparation of cDNA libraries required for subtraction cloning can be performed by using commercially available kit, for example, PCR-Select Subtraction Kit (CLONTECH, cat: K1804-1). The experiment can be performed according to the document of procedure accompanying in the kit.

[0059] An example of practical experimental procedure is listed below, briefly.

[0060] PolyA⁺ RNA is prepared from cells with or without stimulation with appropriate stimulant as previously reported method (Nucleic Acids Res., Vol.26, No.4, p.911-918, 1998). Next, cDNA is prepared using reverse transcriptase from each polyA⁺ RNA samples, as is the commonly used method. cDNA prepared from stimulated cells is used as tester cDNA and that prepared from unstimulated cells as driver cDNA.

[0061] According to the previous report mentioned above and experimental manuals accompanying with kit, driver cDNA is added to tester cDNA to perform subtraction. The efficiency of subtraction is monitored by adding small amount of exogenous DNA as a control. After subtraction, the exogenous DNA is concentrated.

[0062] The subtracted cDNA is cloned into appropriate plasmid expression vector to construct a plasmid library by

commonly used method.

[0063] Similar to the previous report, many colonies are screened by differential hybridization method (Nucleic Acids Res., Vol.26, No.4, p.911-918, 1998; RINSYO-MEN-EKI, Vol.29, No.Suppl.17, p.451-459, 1997). Here, as the hybridization probes, tester cDNA and driver cDNA mentioned above labeled with radioisotope can be used. Clones containing the objective DNA and that containing exogenous DNA can be distinguished by hybridizing the exogenous DNA with replicant filters.

[0064] Objective cDNA or its fragment can be obtained by selecting clones giving strong signal against radiolabeled tester cDNA probe rather than radiolabeled driver cDNA probe.

[0065] Also, cDNA encoding the protein of the present invention can be accomplished by other general cDNA screening method.

[0066] For instance, cDNA or its fragment encoding the protein of the present invention cloned by subtraction cloning method mentioned above, or chemically synthesized oligonucleotides corresponding to amino acid sequence of the protein of the present invention, are labeled with ³²P to make probes, then by well-known colony hybridization method (Crunstein et al., Proc. Natl. Acad. Sci. USA, Vol.72, p.3961, 1975) or plaque hybridization method (Molecular Cloning, A Laboratory Manual, second edition, Cold Spring Harbor Laboratory, p.2.108, 1989), commercial or originally prepared cDNA libraries can be screened. Furthermore, a method to amplify DNA including cDNA encoding the protein of the present invention by PCR, by constructing a pair of PCR primer based on cDNA or its fragment encoding the protein of the present invention isolated by the subtraction cloning mentioned above, can be listed.

[0067] When a cDNA library prepared using a cDNA expression vector is used, the desired clone can be screened by the antigen-antibody reaction using an antibody against the desired protein. A screening method using PCR method is preferably used when many clones are subjected to screening.

[0068] The nucleotide sequence of the DNA thus obtained can be determined by Maxam-Gilbert method (Maxam et al. Proc. Natl. Acad. Sci. USA, Vol.74, p.560 (1977)) or the dideoxynucleotide synthetic chain termination method using phage M13 (Sanger et al. Proc. Natl. Acad. Sci. USA, Vol.74, pp.5463-5467 (1977)). The nucleotide sequence can be easily determined using a commercial DNA sequencer.

[0069] The whole or a part of the gene encoding the protein of the present invention can be obtained by excising the clone obtained as mentioned above with restriction enzymes and so on.

[0070] (2) Also, the DNA encoding the protein of the present invention can be isolated from the genomic DNA derived from the cells expressing the protein of the present invention as mentioned above by the following methods.

[0071] Such cells are solubilized preferably by SDS or proteinase K, and the DNAs are deproteinized by repeating phenol extraction. RNAs are digested preferably with ribonuclease. The DNAs obtained are partially digested with appropriate restriction enzymes, and the DNA fragments obtained are amplified with appropriate phage or cosmid to generate a library. Then, clones having the desired sequence are detected, for example, by using radioactively labeled DNA probes, and the whole or a portion of the gene encoding the protein of the present invention is obtained from the clones by excision with restriction enzymes, etc.

[0072] For example, cDNA encoding a human-derived protein can be obtained by preparing a cosmid library into which human genomic DNAs (chromosomal DNAs) are introduced ("Laboratory Manual Human Genome Mapping," M. Hori and Y. Nakamura, eds., Maruzen), screening the cosmid library to obtain positive clones containing DNA corresponding to the coding region of the desired protein, and screening the above cDNA library using the coding region DNA excised from the positive clones as a probe.

[0073] Also, the present invention relates to any fragment of DNA (cDNA, genomic DNA, etc.) encoding AID protein (especially human AID protein) of the present invention described above. DNA with complementary nucleotide sequence to any nucleotide sequence of cDNA or genomic DNA is useful as a primer DNA in polymerase chain reaction (PCR). By PCR using a pair of the primer DNA, any partial nucleotide sequence of genomic DNA encoding AID protein (especially human AID protein) of the present invention can be amplified.

[0074] For instance, in the case that mutation or deletion of genomic DNA (especially exon) encoding the AID protein is presumed to cause a certain immunodeficiency or allergy, the existence of such the mutation or deletion can be analyzed by PCR described below.

(1) Prepare a pair of primers comprising complementary nucleotide sequence to any partial nucleotide sequence of genomic DNA encoding AID protein of the present invention.

(2) Amplify the objective partial nucleotide sequence of the genomic DNA using the pair of primers, using genomic DNA encoding AID protein obtained from tissue or cells of immunodeficiency or allergy patients as templates.

(3) Analyze the existence of PCR products and the nucleotide sequence of the PCR products, and identify the mutation and deletion in the genomic DNA by comparing the nucleotide sequence and corresponding nucleotide sequence of genomic DNA encoding AID protein derived from normal human.

[0075] Thus, the method described above can not only elucidate, for example, the relation between immunodeficien-

cy and/or allergy and AID protein, but also be used for the diagnosis of a certain kind of disease, in the case that AID protein is the cause of the disease.

[0076] Examples of the nucleotide sequence of the primer DNA are as follows:

5 (1) A DNA comprising a complementary nucleotide sequence to an arbitrary partial sequence of a nucleotide sequence of any one of (a) to (h) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10,
- 10 (c) SEQ ID NO: 11,
- (d) SEQ ID NO: 12,
- (e) SEQ ID NO: 13,
- (f) SEQ ID NO: 14,
- (g) SEQ ID NO: 15, or
- 15 (h) SEQ ID NO: 35.

(2) A DNA comprising a nucleotide sequence of any one of (a) to (q) below:

- (a) SEQ ID NO: 18,
- 20 (b) SEQ ID NO: 19,
- (c) SEQ ID NO: 20,
- (d) SEQ ID NO: 21,
- (e) SEQ ID NO: 22,
- (f) SEQ ID NO: 23,
- 25 (g) SEQ ID NO: 24,
- (h) SEQ ID NO: 25,
- (i) SEQ ID NO: 26,
- (j) SEQ ID NO: 27,
- (k) SEQ ID NO: 28,
- 30 (l) SEQ ID NO: 29,
- (m) SEQ ID NO: 30,
- (n) SEQ ID NO: 31,
- (o) SEQ ID NO: 32,
- (p) SEQ ID NO: 33, or,
- 35 (q) SEQ ID NO: 34.

[0077] Also, the present invention relates to the use of the above-mentioned DNA fragment as a primer DNA in polymerase chain reaction.

40 **[0078]** Examples of the combination of primer DNAs for PCR in diagnosis accomplished by PCR gene amplification and by analyzing it are as follows:

- (1) a DNA comprising the nucleotide sequence of SEQ ID NO: 31 and a DNA comprising the nucleotide sequence of SEQ ID NO: 32,
- 45 (2) a DNA comprising the nucleotide sequence of SEQ ID NO: 20 and a DNA comprising the nucleotide sequence of SEQ ID NO: 22,
- (3) a DNA comprising the nucleotide sequence of SEQ ID NO: 21 and a DNA comprising the nucleotide sequence of SEQ ID NO: 30,
- (4) a DNA comprising the nucleotide sequence of SEQ ID NO: 24 and a DNA comprising the nucleotide sequence of SEQ ID NO: 25,
- 50 (5) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (6) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- 55 (7) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (8) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (9) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence

of SEQ ID NO: 28,

(10) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,

(11) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,

(12) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,

(13) a DNA comprising the nucleotide sequence of SEQ ID NO: 33 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29, or,

(14) a DNA comprising the nucleotide sequence of SEQ ID NO: 18 and a DNA comprising the nucleotide sequence of SEQ ID NO: 19.

[0079] Moreover, the present invention also relates to a recombinant vector comprising the DNA encoding the protein of the present invention. As a recombinant vector of the present invention, any vector can be used as long as it is capable of retaining replication or self-multiplication in each host cell of prokaryotic and/or eukaryotic cells, including plasmid vectors and phage vectors.

[0080] The recombinant vector can easily be prepared by ligating the DNA encoding protein of the present invention with a vector for recombination available in the art (plasmid DNA and bacteriophage DNA) by the usual method.

[0081] Specific examples of the vectors for recombination used are *E. coli*-derived plasmids such as pBR322, pBR325, pUC12, pUC13, and pUC19, yeast-derived plasmids such as pSH19 and pSH15, and *Bacillus subtilis*-derived plasmids such as pUB110, pTP5, and pC194. Examples of phages are a bacteriophage such as λ phage, and an animal or insect virus (pVL1393, Invitrogen) such as a retrovirus, vaccinia virus, and nuclear polyhedrosis virus.

[0082] An expression vector is useful for expressing the DNA encoding the protein of the present invention and for producing the protein of the present invention. The expression vector is not limited as long as it expresses the gene encoding the protein of the present invention in various prokaryotic and/or eukaryotic host cells and produces this protein. Examples thereof are pMAL C2, pEF-BOS (Nucleic Acids Res. Vol.18, p.5322 (1990) and so on), pME18S (Experimental Medicine: SUPPLEMENT, "Handbook of Genetic Engineering" (1992) and so on), etc.

[0083] Also, the protein of the present invention can be produced as a fusion protein with other protein. It can be prepared as a fusion protein, for example, with GST (Glutathione S-transferase) by subcloning a cDNA encoding the protein of the present invention, for example, into plasmid pGEX4T1 (Pharmacia), by transforming *E. coli* DH5 α , and by culturing the transformant.

[0084] When bacteria, particularly *E. coli* are used as host cells, an expression vector generally comprises, at least, a promoter/operator region, an initiation codon, the DNA encoding the protein of the present invention, termination codon, terminator region, and replicon.

[0085] When yeast, animal cells, or insect cells are used as hosts, an expression vector is preferably comprising, at least, a promoter, an initiation codon, the DNA encoding the protein of the present invention, and a termination codon. It may also comprise the DNA encoding a signal peptide, enhancer sequence, 5'- and 3'-untranslated region of the gene encoding the protein of the present invention, splicing junctions, polyadenylation site, selectable marker region, and replicon. The expression vector may also contain, if required, a gene for gene amplification (marker) that is usually used.

[0086] A promoter/operator region to express the protein of the present invention in bacteria comprises a promoter, an operator, and a Shine-Dalgarno (SD) sequence (for example, AAGG). For example, when the host is *Escherichia*, it preferably comprises Trp promoter, lac promoter, recA promoter, λ PL promoter, lpp promoter, tac promoter, or the like. Examples of a promoter to express the protein of the present invention in yeast are PH05 promoter, PGK promoter, GAP promoter, ADH promoter, and so on. When the host is *Bacillus*, examples thereof are SL01 promoter, SP02 promoter, penP promoter, and so on. When the host is a eukaryotic cell such as a mammalian cell, examples thereof are SV40-derived promoter, retrovirus promoter, heat shock promoter, and so on, and preferably SV-40 and retrovirus-derived one. As a matter of course, the promoter is not limited to the above examples. In addition, using an enhancer is effective for expression.

[0087] A preferable initiation codon is, for example, a methionine codon (ATG).

[0088] A commonly used termination codon (for example, TAG, TAA, TGA) is exemplified as a termination codon.

[0089] Usually, used natural or synthetic terminators are used as a terminator region.

[0090] Areplicon means a DNA capable of replicating the whole DNA sequence in host cells, and includes a natural plasmid, an artificially modified plasmid (DNA fragment prepared from a natural plasmid), a synthetic plasmid, and so on. Examples of preferable plasmids are pBR322 or its artificial derivatives (DNA fragment obtained by treating pBR322 with appropriate restriction enzymes) for *E. coli*, yeast 2 μ plasmid or yeast chromosomal DNA for yeast, and pRSVneo ATCC 37198, pSV2dhfr ATCC 37145, pdBPV-MMTneo ATCC 37224, pSV2neo ATCC 37149, and such for mammalian cells.

[0091] An enhancer sequence, polyadenylation site, and splicing junction that are usually used in the art, such as those derived from SV40 can also be used.

[0092] A selectable marker usually employed can be used according to the usual method. Examples thereof are resistance genes for antibiotics, such as tetracycline, ampicillin, or kanamycin.

[0093] Examples of genes for gene amplification are dihydrofolate reductase (DHFR) gene, thymidine kinase gene, neomycin resistance gene, glutamate synthase gene, adenosine deaminase gene, ornithine decarboxylase gene, hygromycin-B-phosphotransferase gene, aspartate transcarbamylase gene, etc.

[0094] The expression vector of the present invention can be prepared by continuously and circularly linking at least the above-mentioned promoter, initiation codon, DNA encoding the protein of the present invention, termination codon, and terminator region, to an appropriate replicon. If desired, appropriate DNA fragments (for example, linkers, restriction sites, and so on), can be used by the usual method such as digestion with a restriction enzyme or ligation using T4 DNA ligase.

[0095] Transformants of the present invention can be prepared by introducing the expression vector mentioned above into host cells.

[0096] Host cells used in the present invention are not limited as long as they are compatible with an expression vector mentioned above and can be transformed. Examples thereof are various cells such as wild-type cells or artificially established recombinant cells usually used in technical field of the present invention (for example, bacteria (*Escherichia* and *Bacillus*), yeast (*Saccharomyces*, *Pichia*, and such), animal cells, or insect cells).

[0097] *E. coli* or animal cells are preferably used. Specific examples are *E. coli* (DH5 α , TB1, HB101, and such), mouse-derived cells (COP, L, C127, Sp2/0, NS-1, NIH 3T3, and such), rat-derived cells (PC12, PC12h), hamster-derived cells (BHK, CHO, and such), monkey-derived cells (COS1, COS3, COS7, CV1, Velo, and such), and human-derived cells (Hela, diploid fibroblast-derived cells, myeloma cells, and HepG2, and such).

[0098] An expression vector can be introduced (transformed (transfected)) into host cells by known methods.

[0099] Transformation can be performed, for example, according to the method of Cohen et al. (Proc. Natl. Acad. Sci. USA, Vol.69, p.2110 (1972)), protoplast method (Mol. Gen. Genet., Vol.168, p.111 (1979)), or competent method (J. Mol. Biol., Vol.56, p.209 (1971)) when the hosts are bacteria (*E. coli*, *Bacillus subtilis*, and such), the method of Hinnen et al. (Proc. Natl. Acad. Sci. USA, Vol.75, p.1927 (1978)), or lithium method (J. Bacteriol., Vol.153, p.163 (1983)) when the host is *Saccharomyces cerevisiae*, the method of Graham (Virology, Vol.52, p.456 (1973)) when the hosts are animal cells, and the method of Summers et al. (Mol. Cell. Biol., Vol.3, pp.2156-2165 (1983)) when the hosts are insect cells.

[0100] The protein of the present invention can be produced by cultivating transformants (in the following, this term includes transfectants) comprising an expression vector prepared as mentioned above in nutrient media.

[0101] The nutrient media preferably comprise carbon source, inorganic nitrogen source, or organic nitrogen source necessary for the growth of host cells (transformants). Examples of the carbon source are glucose, dextran, soluble starch, and sucrose, and examples of the inorganic or organic nitrogen source are ammonium salts, nitrates, amino acids, corn steep liquor, peptone, casein, meat extract, soy bean cake, and potato extract. If desired, they may comprise other nutrients (for example, an inorganic salt (for example, calcium chloride, sodium dihydrogenphosphate, and magnesium chloride), vitamins, antibiotics (for example, tetracycline, neomycin, ampicillin, kanamycin, and so on).

[0102] Cultivation is performed by a method known in the art. Cultivation conditions such as temperature, pH of the media, and cultivation time are selected appropriately so that the protein of the present invention is produced in large quantities.

[0103] Specific media and cultivation conditions used depending on host cells are illustrated below, but are not limited thereto.

[0104] When the hosts are bacteria, actinomycetes, yeasts, filamentous fungi, liquid media comprising the nutrient source mentioned above are appropriate. The media with pH 5 to 8 are preferably used.

[0105] When the host is *E. coli*, examples of preferable media are LB media, M9 media (Miller et al. Exp. Mol. Genet., Cold Spring Harbor Laboratory, p.431 (1972)), and so on. Using these media, cultivation can be performed usually at 14 to 43°C for about 3 to 24 hours with aeration and stirring, if necessary.

[0106] When the host is *Bacillus*, cultivation can be performed usually at 30 to 40°C for about 16 to 96 hours with aeration and stirring, if necessary.

[0107] When the host is yeast, an example of media is Burkholder minimal media (Bostian, Proc. Natl. Acad. Sci. USA, Vol.77, p.4505 (1980)). The pH of the media is preferably 5 to 8. Cultivation can be performed usually at 20 to 35°C for about 14 to 144 hours with aeration and stirring, if necessary.

[0108] When the host is an animal cell, examples of media are MEM media containing about 5 to 20% fetal bovine serum (Science, Vol.122, p.501 (1952)), DMEM media (Virology, Vol.8, p.396 (1959)), RPMI1640 media (J. Am. Med. Assoc., Vol.199, p.519 (1967)), 199 media (Proc. Soc. Exp. Biol. Med., Vol.73, p.1 (1950)), and so on. The pH of the media is preferably about 6 to 8. Cultivation can be performed usually at about 30 to 40°C for about 15 to 72 hours with aeration and stirring, if necessary.

[0109] When the host is an insect cell, an example of media is Grace's media containing fetal bovine serum (Proc. Natl. Acad. Sci. USA, Vol.82, p.8404 (1985)). The pH thereof is preferably about 5 to 8. Cultivation can be performed usually at about 20 to 40°C for 15 to 100 hours with aeration and stirring, if necessary.

[0110] The protein of the present invention can be produced by cultivating transformants, especially mammalian cells, as mentioned above and allowing them to secrete the protein into the culture supernatant.

[0111] A culture filtrate (supernatant) is obtained by a method such as filtration or centrifugation of the obtained culture, and the protein of the present invention is purified and isolated from the culture filtrate by methods commonly used in order to purify and isolate a natural or synthetic protein.

[0112] Examples of the isolation and purification method are a method utilizing solubility, such as salting out and solvent precipitation method; a method utilizing the difference in molecular weight, such as dialysis, ultrafiltration, gel filtration, and sodium dodecyl sulfate-polyacrylamide gel electrophoresis; a method utilizing charges, such as ion exchange chromatography and hydroxylapatite chromatography; a method utilizing specific affinity, such as affinity column chromatography; a method utilizing the difference in hydrophobicity, such as reverse phase high performance liquid chromatography; and a method utilizing the difference in isoelectric point, such as isoelectric focusing.

[0113] When the protein of the present invention exists in the periplasm or cytoplasm of cultured transformants (for example, *E. Coli*), first, the cells are harvested by a usual method such as filtration or centrifugation and suspended in appropriate buffer. After the cell wall and/or cell membrane of the cells and such are disrupted by the method such as lysis with sonication, lysozyme, and freeze-thawing, the membrane fraction comprising the protein of the present invention is obtained by the method such as centrifugation or filtration. The membrane fraction is solubilized with a detergent such as Triton-X100 to obtain the crude extract. Finally, the protein is isolated and purified from the crude extract by the usual method as illustrated above.

[0114] By using a DNA (cDNA or genomic DNA) encoding a human-derived AID protein included in the protein of the present invention, transgenic non-human mammals secreting the human AID protein in their body can be prepared. Namely, by integrating the human-derived DNA into an endogenous locus of non-human mammals (e.g. mouse), the human AID protein of the present invention encoded by the DNA is expressed and secreted in their body. The transgenic non-human mammals are included in the present invention.

[0115] The transgenic non-human mammals can be prepared according to the method usually used for producing a transgenic animal (for example, see "Newest Manual of Animal Cell Experiment", LIC press, Chapter 7, pp.361-408, (1990)).

[0116] Specifically, for example, a transgenic mouse can be produced as follows. Embryonic stem cells (ES cells) obtained from normal mouse blastocysts are transformed with an expression vector in which the gene encoding the human AID protein of the present invention and a marker gene (for example, neomycin resistance gene) have been inserted in an expressible manner. ES cells in which the gene encoding the human AID protein of the present invention has been integrated into the endogenous gene are screened by a usual method based on expression of the marker gene. Then, the ES cells screened are microinjected into a fertilized egg (blastocyst) obtained from another normal mouse (Proc. Natl. Acad. Sci. USA, Vol.77, No.12, pp.7380-7384 (1980); U.S. Pat. No. 4,873,191).

[0117] The blastocyst is transplanted into the uterus of another normal mouse as the foster mother. Then, founder mice are born from the foster mother. By mating the founder mice with normal mice, heterozygous transgenic mice are obtained. By mating the heterozygous transgenic mice with each other, homozygous transgenic mice are obtained according to Mendel's laws.

[0118] Also, so-called "knockout mouse" can be generated based on the nucleotide sequence of DNA encoding mouse AID protein included in the present invention. The "knockout mouse" in the present invention means the mouse in which the endogenous gene encoding the mouse AID protein of the present invention is knocked-out (inactivated). For example, it can be generated by positive-negative selection method applying homologous recombination (U.S. Pat. No. 5,464,764; 5,487,992; 5,627,059; Proc. Natl. Acad. Sci. USA, Vol.86, 8932-8935, 1989, Nature, Vol.342, 435-438, 1989; etc.), and such knockout mice are one embodiment of the present invention.

[0119] The "antibody" in the present invention means a polyclonal antibody (antiserum) or a monoclonal antibody, and preferably a monoclonal antibody.

[0120] Specifically, it includes an antibody reactive to the above-mentioned protein of the present invention and a fragment thereof.

[0121] The "antibody" of the present invention also includes a natural antibody that can be prepared by immunizing mammals such as mice, rats, hamsters, guinea pigs, or rabbits with the protein of the present invention (including natural, recombinant, and chemically synthesized protein and cell), a fragment thereof, or a transformant highly expressing the protein of interest by recombinant technology mentioned above; a chimeric antibody and a humanized antibody (CDR-grafted antibody) that can be produced by recombinant technology; and a human monoclonal antibody that can be produced by using human antibody-producing transgenic animals.

[0122] The monoclonal antibody includes those having any one of the isotypes of IgG, IgM, IgA, IgD, or IgE. IgG or IgM is preferable.

[0123] The polyclonal antibody (antiserum) or monoclonal antibody of the present invention can be produced by known methods. Namely, mammals, preferably, mice, rats, hamsters, guinea pigs, rabbits, cats, dogs, pigs, goats, horses, or bovine, or more preferably, mice, rats, hamsters, guinea pigs, or rabbits are immunized, for example, with an antigen mentioned above with Freund's adjuvant, if necessary. The polyclonal antibody can be obtained from the serum obtained from the animal so immunized. The monoclonal antibodies are produced as follows. Hybridomas are produced by fusing the antibody-producing cells obtained from the animal so immunized and myeloma cells incapable of producing autoantibodies. Then the hybridomas are cloned, and clones producing the monoclonal antibodies showing the specific affinity to the antigen used for immunizing the mammal are screened.

[0124] Specifically, the monoclonal antibody can be produced as follows. Immunizations are done by injecting or implanting once or several times the above-mentioned protein of the present invention, a fragment thereof, the cells that express the protein, and so on as an immunogen, if necessary, with Freund's adjuvant, subcutaneously, intramuscularly, intravenously, through the footpad, or intraperitoneally into mice, rats, hamsters, guinea pigs, or rabbits, preferably mice, rats or hamsters (including transgenic animals generated so as to produce antibodies derived from another animal such as the transgenic mouse producing human antibody). Usually, immunizations are performed once to four times every one to fourteen days after the first immunization. Antibody-producing cells are obtained from the mammal so immunized in about one to five days after the last immunization.

[0125] Hybridomas that secrete a monoclonal antibody can be prepared by the method of Köhler and Milstein (Nature, Vol.256, pp.495-497 (1975)) and by its modified method. Namely, hybridomas are prepared by fusing antibody-producing cells contained in a spleen, lymph node, bone marrow, or tonsil obtained from the non-human mammal immunized as mentioned above, preferably a spleen, with myeloma cells without autoantibody-producing ability, which are derived from, preferably, a mammal such as mice, rats, guinea pigs, hamsters, rabbits, or humans, or more preferably, mice, rats, or humans.

[0126] For example, mouse-derived myeloma P3/X63-AG8.653 (653; ATCC No. CRL1580), P3/NSI/1-Ag4-1 (NS-1), P3/X63-Ag8.U1 (P3U1), SP2/0-Ag14 (Sp2/0, Sp2), PAI, F0, or BW5147; rat-derived myeloma 210RCY3-Ag.2.3.; or human-derived myeloma U-266AR1, GM1500-6TG-A1-2, UC729-6, CEM-AGR, D1R11, or CEM-T15 can be used as a myeloma used for the cell fusion.

[0127] Hybridoma clones producing monoclonal antibodies can be screened by cultivating the hybridomas, for example, in microtiter plates and by measuring the reactivity of the culture supernatant in the well in which hybridoma growth is observed, to the immunogen used for the immunization mentioned above, for example, by an enzyme immunoassay such as RIA and ELISA.

[0128] The monoclonal antibodies can be produced from hybridomas by cultivating the hybridomas *in vitro* or *in vivo* such as in the ascites of mice, rats, guinea pigs, hamsters, or rabbits, preferably mice or rats, more preferably mice and isolating the antibodies from the resulting the culture supernatant or ascites fluid of a mammal.

[0129] *In vitro* cultivation can be performed depending on the property of cells to be cultured, on the object of a test study, and on various culture, by using known nutrient media or any nutrient media derived from known basal media for growing, maintaining, and storing the hybridomas to produce monoclonal antibodies in the culture supernatant.

[0130] Examples of basal media are low calcium concentration media such as Ham's F12 medium, MCDB153 medium, or low calcium concentration MEM medium, and high calcium concentration media such as MCDB104 medium, MEM medium, D-MEM medium, RPMI1640 medium, ASF104 medium, or RD medium. The basal media can contain, for example, sera, hormones, cytokines, and/or various inorganic or organic substances depending on the objective.

[0131] Monoclonal antibodies can be isolated and purified from the culture supernatant or ascites mentioned above by saturated ammonium sulfate precipitation, euglobulin precipitation method, caproic acid method, caprylic acid method, ion exchange chromatography (DEAE or DE52), affinity chromatography using anti-immunoglobulin column or protein A column.

[0132] Furthermore, monoclonal antibodies can be obtained in a large quantity by cloning a gene encoding a monoclonal antibody from the hybridoma, generating transgenic bovines, goats, sheep, or pigs in which the gene encoding the antibody is integrated in its endogenous gene using transgenic animal generating technique, and recovering the monoclonal antibody derived from the antibody gene from milk of the transgenic animals (Nikkei Science, No.4, pp. 78-84 (1997)).

[0133] The "chimeric antibody" of the present invention means a monoclonal antibody prepared by genetic engineering, and specifically, a chimeric monoclonal antibody, for example, mouse/human chimeric antibody, whose variable region is a mouse immunoglobulin-derived variable region and whose constant region is a human immunoglobulin-derived constant region.

[0134] The constant region derived from human immunoglobulin has the amino acid sequence inherent in each isotype such as IgG, IgM, IgA, IgD, IgE, etc. The constant region of the recombinant chimeric monoclonal antibody of the present invention can be that of human immunoglobulin belonging to any isotype. Preferably, it is the constant region of human IgG.

[0135] The chimeric monoclonal antibody of the present invention can be produced, for example, as follows. Needless

to say, the production method is not limited thereto.

[0136] For example, mouse/human chimeric monoclonal antibody can be prepared, by referring to Experimental Medicine: SUPPLEMENT, Vol.1.6, No.10 (1988); and Examined Published Japanese Patent Application (JP-B) No. Hei 3-73280. Namely, it can be prepared by ligating C_H gene (C gene encoding the constant region of H chain) obtained from the DNA encoding human immunoglobulin to the downstream of active V_H genes (rearranged VDJ gene encoding the variable region of H chain) obtained from the DNA encoding mouse monoclonal antibody isolated from the hybridoma producing the mouse monoclonal antibody, and by ligating the C_L gene (C gene encoding the constant region of L chain) obtained from the DNA encoding human immunoglobulin to the downstream of active V_L genes (rearranged VJ gene encoding the variable region of L chain) obtained from the DNA encoding the mouse monoclonal antibody isolated from the hybridoma, and operably inserting those into the same or different vectors in an expressible manner, followed by transformation of host cells with the expression vector, and cultivation of the transformants.

[0137] Specifically, DNAs are first extracted from mouse monoclonal antibody-producing hybridoma by the usual method, digested with appropriate restriction enzymes (for example, EcoRI and HindIII), electrophoresed (using, for example, 0.7% agarose gel), and analyzed by Southern blotting. After the electrophoresed gel is stained, for example, with ethidium bromide and photographed, the gel is given marker positions, washed twice with water, and soaked in 0.25 M HCl for 15 minutes. Then, the gel is soaked in 0.4 N NaOH solution for 10 minutes with gentle stirring. The DNAs are transferred to a filter for 4 hours following the usual method. The filter is recovered and washed twice with 2 x SSC. After the filter is sufficiently dried, it is baked at 75°C for 3 hours, treated with 0.1 x SSC/0.1% SDS at 65°C for 30 minutes, and then soaked in 3 x SSC/0.1% SDS. The filter obtained is treated with prehybridization solution in a plastic bag at 65°C for 3 to 4 hours.

[0138] Next, ³²P-labeled probe DNA and hybridization solution are added to the bag and reacted at 65°C about 12 hours. After hybridization, the filter is washed under an appropriate salt concentration, reaction temperature, and time (for example, 2 x SSC/0.1% SDS, room temperature, 10 minutes). The filter is put into a plastic bag with a little 2 x SSC, and subjected to autoradiography after the bag is sealed.

[0139] Rearranged VDJ gene and VJ gene encoding H chain and L chain of mouse monoclonal antibody respectively are identified by Southern blotting mentioned above. The region comprising the identified DNA fragment is fractionated by sucrose density gradient centrifugation and inserted into a phage vector (for example, Charon 4A, Charon 28, λEMBL3, λEMBL4, etc.). *E. coli* (for example, LE392, NM539, etc.) are transformed with the phage vector to generate a genomic library. The genomic library is screened by plaque hybridization such as the Benton-Davis method (Science, Vol.196, pp.180-182 (1977)) using appropriate probes (H chain J gene, L chain (κ) J gene, etc.) to obtain positive clones comprising rearranged VDJ gene or VJ gene respectively. By making the restriction map and determining the nucleotide sequence of the clones obtained, it is confirmed that genes comprising the desired, rearranged V_H (VDJ) gene or V_L (VJ) gene have been obtained.

[0140] Separately, human C_H gene and human C_L gene used for chimerization are isolated. For example, when a chimeric antibody with human IgG1 is produced, C_γ1 gene is isolated as a C_H gene, and C_κ gene is also isolated as a C_L gene, are isolated. These genes can be isolated from human genomic library with mouse C_γ1 gene and mouse C_κ gene, corresponding to human C_γ1 gene and human C_κ gene, respectively, as probes, taking advantage of the high homology between the nucleotide sequences of mouse immunoglobulin gene and that of human immunoglobulin gene.

[0141] Specifically, DNA fragments comprising human C_κ gene and an enhancer region are isolated from human λ Charon 4A HaeIII-AluI genomic library (Cell, Vol.15, pp.1157-1174 (1978)), for example, using a 3 kb HindIII-BamHI fragment from clone Ig146 (Proc. Natl. Acad. Sci. USA, Vol.75, pp.4709-4713 (1978)) and a 6.8 kb EcoRI fragment from clone MEP10 (Proc. Natl. Acad. Sci. USA, Vol.78, pp.474-478 (1981)) as probes. In addition, for example, after human fetal hepatocyte DNA is digested with HindIII and fractioned by agarose gel electrophoresis, a 5.9 kb fragment is inserted into λ788 and then human C_γ1 gene is isolated with the probes mentioned above.

[0142] Using mouse V_H gene, mouse V_L gene, human C_H gene, and human C_L gene so obtained, and taking promoter region and enhancer region into consideration, human C_H gene is inserted downstream of mouse V_H gene and human C_L gene is inserted downstream of mouse V_L gene in an expression vector such as pSV2gpt or pSV2neo with appropriate restriction enzymes and DNA ligase following the usual method. In this case, chimeric genes of mouse V_H gene/human C_H gene and mouse V_L gene/human C_L gene can be respectively inserted into a same or different expression vector.

[0143] Chimeric gene-inserted expression vector(s) thus prepared are introduced into myeloma cells (e.g., P3X63 Ag8 653 cells or SP210 cells) that do not produce antibodies by the protoplast fusion method, DEAE-dextran method, calcium phosphate method, or electroporation method. The transformants are screened by cultivating in a medium containing a drug corresponding to the drug resistance gene inserted into the expression vector and, then, cells producing desired chimeric monoclonal antibodies are obtained.

[0144] Desired chimeric monoclonal antibodies are obtained from the culture supernatant of antibody-producing cells thus screened.

[0145] The "humanized antibody (CDR-grafted antibody)" of the present invention is a monoclonal antibody prepared by genetic engineering and specifically means a humanized monoclonal antibody wherein a portion or the whole of the complementarity determining regions of the hyper-variable region are derived from those of the hyper-variable region from mouse monoclonal antibody, the framework regions of the variable region are derived from those of the variable region from human immunoglobulin, and the constant region is derived from that from human-immunoglobulin.

[0146] The complementarity determining regions of the hyper-variable region exists in the hyper-variable region in the variable region of an antibody and means three regions which directly binds, in a complementary manner, to an antigen (complementarity-determining residues, CDR1, CDR2, and CDR3). The framework regions of the variable region mean four comparatively conserved regions intervening upstream, downstream or between the three complementarity-determining regions (framework region, FR1, FR2, FR3, and FR4).

[0147] In other words, a humanized monoclonal antibody means that in which the whole region except a portion or the whole region of the complementarity determining regions of the hyper-variable region of a mouse monoclonal antibody has been replaced with their corresponding regions derived from human immunoglobulin.

[0148] The constant region derived from human immunoglobulin has the amino acid sequence inherent in each isotype such as IgG, IgM, IgA, IgD, and IgE. The constant region of a humanized monoclonal antibody in the present invention can be that from human immunoglobulin belonging to any isotype. Preferably, it is the constant region of human IgG. The framework regions of the constant region derived from human immunoglobulin are not particularly limited.

[0149] The humanized monoclonal antibody of the present invention can be produced, for example, as follows. Needless to say, the production method is not limited thereto.

[0150] For example, a recombinant humanized monoclonal antibody derived from mouse monoclonal antibody can be prepared by genetic engineering, referring to Published Japanese Translations of PCT International Publication No. Hei 4-506458 and Unexamined Published Japanese Patent Application (JP-A) No. Sho 62-296890. Namely, at least one mouse H chain CDR gene and at least one mouse L chain CDR gene corresponding to the mouse H chain CDR gene are isolated from hybridomas producing mouse monoclonal antibody, and human H chain gene encoding the whole region except human H chain CDR corresponding to mouse H chain CDR mentioned above and human L chain gene encoding the whole region except human L chain CDR corresponding to mouse L chain CDR mentioned above are isolated from human immunoglobulin genes.

[0151] The mouse H chain CDR gene(s) and the human H chain gene(s) so isolated are inserted, in an expressible manner, into an appropriate vector so that they can be expressed. Similarly, the mouse L chain CDR gene(s) and the human L chain gene (s) are inserted, in an expressible manner, into another appropriate vector so that they can be expressed. Alternatively, the mouse H chain CDR gene(s)/human H chain gene(s) and mouse L chain CDR gene(s)/human L chain gene(s) can be inserted, in an expressible manner, into the same expression vector so that they can be expressed. Host cells are transformed with the expression vector thus prepared to obtain transformants producing humanized monoclonal antibody. By cultivating the transformants, desired humanized monoclonal antibody is obtained from culture supernatant.

[0152] The "human antibody" used in the present invention is immunoglobulin in which the entire regions comprising the variable and constant region of H chain, and the variable and constant region of L chain constituting immunoglobulin are derived from the genes encoding human immunoglobulin.

[0153] The human antibody can be produced in the same way as the production method of polyclonal or monoclonal antibodies mentioned above by immunizing, with an antigen, a transgenic animal which for example, at least human immunoglobulin gene(s) have been integrated into the locus of a non-human mammal such as a mouse by the usual method.

[0154] For example, a transgenic mouse producing human antibodies is prepared by the methods described in already published literatures (Nature Genetics, Vol.7, pp.13-21 (1994); Nature Genetics, Vol.15, pp.146-156 (1997); JP-WA Hei 4-504365; WO94/25585; Nikkei Science, No.6, pp.40-50 (1995); WO94/25585; Nature, Vol.368, pp. 856-859 (1994); JP-WA No. Hei 6-500233).

[0155] The "portion of an antibody" used in the present invention means a partial region of the antibody, and preferably the monoclonal antibody of the present invention as mentioned above, and specifically, means $F(ab')_2$, Fab' , Fab , Fv (variable fragment of antibody), sFv , $dsFv$ (disulfide stabilized Fv), or dAb (single domain antibody) (Exp. Opin. Ther. Patents, Vol.6, No.5, pp.441-456 (1996)).

[0156] " $F(ab')_2$ " and " Fab " can be produced by treating immunoglobulin (monoclonal antibody) with a protease such as pepsin and papain, and means an antibody fragment generated by digesting immunoglobulin near the disulfide bonds existing between the hinge regions in each of the two H chains. For example, papain cleaves IgG upstream of the disulfide bonds existing between the hinge regions in each of the two H chains to generate two homologous antibody fragments in which an L chain composed of V_L (L chain variable region) and C_L (L chain constant region), and an H chain fragment composed of V_H (H chain variable region) and $C_H\gamma 1$ ($\gamma 1$ region in the constant region of H chain) are connected at their C terminal regions through a disulfide bond. Each of these two homologous antibody fragments is

called Fab'. Pepsin also cleaves IgG downstream of the disulfide bonds existing between the hinge regions in each of the two H chains to generate an antibody fragment slightly larger than the fragment in which the two above-mentioned Fab' are connected at the hinge region. This antibody fragment is called F(ab')₂.

[0157] The "cell producing a monoclonal antibody reactive to a protein or a fragment thereof" of the present invention means any cell producing the above-described monoclonal antibody of the present invention.

[0158] More specifically, the following is included:

(1) B cells that are obtained by immunizing the non-human mammals with the above-mentioned protein of the present invention, a fragment thereof, or the cells producing the protein and that produce a monoclonal antibody reactive to the protein of the present invention or a fragment thereof.

(2) The above-mentioned hybridomas (fused cell) prepared by fusing the thus-obtained B cells producing the antibody with myeloma cells derived from mammals.

(3) Monoclonal antibody-producing transformants obtained by transforming other cells than the monoclonal antibody-producing B cells and hybridomas with genes encoding the monoclonal antibody isolated from the monoclonal antibody-producing B cells or hybridomas (either the heavy chain-encoding gene or the light chain-encoding gene, or both).

[0159] The monoclonal antibody-producing transformants of (3) mean recombinant cells producing a recombinant monoclonal antibody produced by B cells of (1) or hybridomas of (2). These antibody producing-transformants can be produced by the method as used for producing the above-described chimeric monoclonal antibody and humanized monoclonal antibody.

[0160] The "pharmaceutical composition" used herein means a pharmaceutical composition comprising of any of the protein, fragment thereof, antibody, or portion thereof defined hereinabove, and a pharmaceutically acceptable carrier.

[0161] The "pharmaceutically acceptable carrier" includes an excipient, a diluent, an expander, a disintegrating agent, a stabilizer, a preservative, a buffer, an emulsifier, an aromatic, a colorant, a sweetener, a viscosity-increasing agent, a flavor, a dissolving agent, or other additives. Using one or more of such carriers, a pharmaceutical composition can be formulated into tablets, pills, powders, granules, injections, solutions, capsules, troches, elixirs, suspensions, emulsions, or syrups. The pharmaceutical composition can be administered orally or parenterally. Other forms for parenteral administration include a solution for external application, suppository for rectal administration, and pessary, prescribed by the usual method, which comprises one or more active ingredient.

[0162] The dosage can vary depending on the age, sex, weight, and symptoms of a patient, effect of treatment, administration route, period of treatment, or the kind of active ingredient (protein or antibody mentioned above) contained in the pharmaceutical composition. Usually, the pharmaceutical composition can be administered to an adult in a dose of 10 µg to 1000 mg (or 10 µg to 500 mg) per one administration. Depending on various conditions, the lower dosage may be sufficient in some cases, and a higher dosage may be necessary in other cases.

[0163] In particular, the injection can be produced by dissolving or suspending the antibody in a non-toxic, pharmaceutically acceptable carrier such as physiological saline or commercially available distilled water for injections by adjusting the concentration to 0.1 µg antibody/ml carrier to 10 mg antibody/ml carrier. The injection thus produced can be administered to a human patient in need of treatment in a dose of 1 µg to 100 mg/kg body weight, preferably 50 µg to 50 mg/kg body weight, once or more times a day. Examples of administration routes are medically appropriate administration routes such as intravenous injection, subcutaneous injection, intradermal injection, intramuscular injection, or intraperitoneal injection, preferably intravenous injection.

[0164] The injection can also be prepared into a non-aqueous diluent (for example, propylene glycol, polyethylene glycol, vegetable oil such as olive oil, and alcohols such as ethanol), suspension, or emulsion.

[0165] The injection can be sterilized by filtration with a bacteria-non-penetrable filter, by mixing bactericide, or by irradiation. The injection can be prepared at the time of use. Namely, it is freeze-dried to make a sterile solid composition, and can be dissolved in sterile distilled water for injection or another solvent before use.

[0166] The pharmaceutical composition of the present invention is useful as a drug for preventing and treating, for example, primary immunodeficiency syndrome with congenital disorder of immune system, mainly immunodeficiency considered to develop by B lymphocyte deficiency, decrease, or dysfunction (e.g., sex-linked agammaglobulinemia, sex-linked agammaglobulinemia with growth hormone deficiency, immunoglobulin deficiency with high IgM level, selective IgM deficiency, selective IgE deficiency, immunoglobulin heavy chain gene deletion, κ chain deficiency, IgA deficiency, IgG subclass selective deficiency, CVID (common variable immunodeficiency), infantile transient dysgammaglobulinemia, Rosen syndrome, severe combined immunodeficiency (sex-linked, autosomal recessive), ADA (adenosine deaminase) deficiency, PNP (purine nucleoside phosphorylase) deficiency, MHC class II deficiency, reticular dysplasia, Wiskott-Aldrich syndrome, ataxia telangiectasia, DiGeorge syndrome, chromosomal aberration, familial Ig hypermetabolism, hyper IgE syndrome, Gitlin syndrome, Nezelof syndrome, Good syndrome, osteodystrophy, transco-

balamin syndrome, secretory bead syndrome, etc.), various diseases with antibody production deficiency that are secondary immunodeficiency syndrome with disorder of immune system caused by an acquired etiology (for example, AIDS, etc.), and/or various allergic diseases (e.g., bronchial asthma, atopic dermatitis, conjunctivitis, allergic rhinitis, allergic enteritis, drug-induced allergy, food allergy, allergic urticaria, glomerulonephritis, etc.), and for reliving condition

due to various immunodeficiency with the diseases.

[0167] The DNA of the present invention described above, namely, "DNA comprising any partial nucleotide sequence of SEQ ID NO: 7, from SEQ ID NO: 9 to SEQ ID NO: 15, SEQ ID NO: 35, those with partial chemical modification, DNA comprising complementary nucleotide sequences to the partial sequence, or those with partial chemical modification" are included.

[0168] Here, the "partial nucleotide sequence" means the partial nucleotide sequence comprising any number of bases at any region included in any nucleotide sequence listed in SEQ ID NO: 7, from SEQ ID NO: 9 to SEQ ID NO: 15, or SEQ ID NO: 35.

[0169] The DNA is useful as probes in DNA hybridization or RNA hybridization procedures. In the purpose of using the DNA as a probe, continuous nucleotide sequence of over 20 bases, preferably continuous nucleotide sequence of over 50 bases, more preferably over 100 bases, much more preferably over 200 bases, especially preferably over 300 bases, can be listed as the partial nucleotide sequences.

[0170] Also, the DNA described above as mentioned before, are useful as primers for PCR. In the purpose of using the DNA as PCR primers, continuous partial nucleotide sequence of from 5 to 100 bases, preferably from 5 to 70 bases, more preferably from 5 to 50 bases, much more preferably from 5 to 30 bases, can be listed as the partial nucleotide sequences.

[0171] Moreover, the DNA described above are useful as antisense drug. The DNA, hybridizing to a DNA or an RNA encoding the AID protein of the present invention, can inhibit transcription of the DNA to mRNA or translation of the mRNA into the protein.

[0172] In purpose of using above-mentioned DNA to antisense drug, the partial nucleotide sequence consists of 5 to 100 consecutive nucleotides, preferably 5 to 70 consecutive nucleotides, more preferably 5 to 50 consecutive nucleotides, and still more preferably 5 to 30 consecutive nucleotides.

[0173] When the DNA is used as an antisense DNA pharmaceutical, the DNA sequence can be modified chemically in part for extending the half-life (stability) of the blood concentration of the DNA administered to patients, for increasing the intracellular-membrane permeability of the DNA, or for increasing the degradation resistance or the absorption of the orally administered DNA in the digestive organs. The chemical modification includes, for example, the modification of the phosphate bonds, the riboses, the nucleotide bases, the sugar moiety, the 3' end and/or the 5' end in the structure of the oligonucleotide DNA.

[0174] The modification of phosphate bond includes, for example, the conversion of one or more of the bonds to phosphodiester bonds (D-oligo), phosphorothioate bonds, phosphorodithioate bonds (S-oligo), methyl phosphonate (MP-oligo), phosphoroamidate bonds, non-phosphate bonds or methyl phosphonothioate bonds, or combinations thereof. The modification of the ribose includes, for example, the conversion to 2'-fluororibose or 2'-O-methylribose. The modification of the nucleotide base includes, for example, the conversion to 5-propynyluracil or 2-aminoadenine.

[0175] Also, another one of the present invention relates to "methods of identifying substances regulating the production of the AID protein of the present invention or the transcription of the gene encoding AID protein to mRNA". The method of the present invention is namely "the method of screening of drugs capable of regulating functions of AID protein or AID gene".

[0176] As the cells used in the method of the present invention, any cells, as long as capable of producing AID protein of the present invention, can be used. For instance, native cells (preferably of mouse or human), transgenic cells transformed with a gene encoding AID protein of the present invention, cells introduced with RNA encoding AID protein of the present invention, etc., can be listed.

[0177] As the host cells used for preparing the transgenic cells, various cells, mentioned in the part explaining in detail on the method of expressing the protein of the present invention using the DNA of the protein described above, can be used.

[0178] For instance, various cells such as naturally established cells or artificially established transgenic cells (e.g. bacteria (*Escherichia*, *Bacillus*), yeast (*Saccharomyces*, *Pichia*), animal cells and insect cells) can be exemplified.

[0179] Preferably, animal cells, namely, cells derived from mouse (COP, L, C127, Sp2/0, NS-1, or NIH3T3, etc.), cells derived from rat (PC12, PC12h, etc.), cells derived from hamster (BHK, and CHO, etc.), cells derived from monkey (COS1, COS3, COS7, CV1, and Velo, etc.), and cells derived from human (Hela, cells derived from diploid fibroblast, HEK293 cells, myeloma cells, and Namalwa, etc.) can be exemplified.

[0180] The "substance" in the present invention means natural substance existing in the nature and any substance prepared artificially. The substances can be grouped into "peptidic substance" and "non-peptidic substance".

[0181] As the "non-peptidic substance", "DNA comprising partial nucleotide sequence, or chemically modified DNA derived from it" that are useful as antisense drug as described above, "antisense RNA" with similar structural and

pharmacological property to the antisense DNA, or any chemically synthesized "compounds" can be exemplified. The "compounds" herein means compounds excepting DNA, RNA, and peptidic substances. Namely, compounds with molecular weight of smaller than from 100 to approximately 1000, preferably compounds with molecular weight of from 100 to 800, more preferably molecular weight of from 100 to 600, can be exemplified.

[0182] As the "peptidic substance", antibodies already described above in detail (preferably monoclonal antibodies, more preferably recombinant antibodies or human monoclonal antibodies), oligopeptides, or chemically modified substance derived from them can be exemplified. Examples of an oligopeptide are a peptide comprising 5 to 30 amino acids, preferably 5 to 20 amino acids. The chemical modification can be designed depending on various purposes, for example, the increased half-life in blood in the case of administering *in vivo*, or the increased tolerance against the degradation or increased absorption in digestive tract at the oral administration.

[0183] Methods described in from (24) to (28) above includes so-called reporter gene assay, as one of the method of the present invention.

[0184] As the "reporter protein", luciferase derived from firefly or sea pansy, or GFP derived from jerryfish, are preferred.

[0185] As the "reporter gene assay", methods described below are representative.

[0186] Transgenic cells are generated by transforming cells commonly used in the production of recombinant proteins with expression vector, in which a gene encoding the target protein and a gene encoding the reporter protein are inserted to the vector so that the transcription of the gene encoding the reporter protein to mRNA occurs dependently on the signal of the transcription of the gene of target protein to mRNA. The test substances (described above) are applied to the obtained transformant cells. Analysis that whether the compound affects the expression of transporter molecule can be accomplished by measuring the level of the target protein by indirect measuring of the amount of fluorescence emitted by the reporter protein expressed in parallel with the target protein (for reference, see U.S. Pat. No. 5,436,128 and U.S. Pat. No. 5,401,629).

[0187] Also, the identification of the compounds using the present assay can be accomplished by manual operation, but it can also be readily and simply done automatically by using so-called High-Throughput Screening using robots (SOSHIKI BAIYO KOUGAKU, Vol.23, No.13, p.521-524; U.S. Pat. No. 5,670,113).

[0188] The "cells" and "substances" used in the methods described above contain the same meaning as defined above.

[0189] The substances identified by the methods of the present invention are very useful as drug for therapy of various diseases considered to be caused by the hyperfunction or deficiency of the AID protein of the present invention or by the deficiency or mutation of the AID gene, or for remission of various symptoms supervene with the diseases.

Brief Description of the Drawings

[0190] Figure 1 is the photograph which shows the production state DNA including an S α sequence looped out with the class switch recombination in mouse B cell clone CH12F3-2 cultured under the various conditions.

[0191] Figure 1 (a) shows the electrophoretic state of DNA including an S α sequence looped out with class switch recombination, amplified by PCR using DNA derived from mouse B cell clone CH12F3-2 cultured under the various conditions.

[0192] Lanes 1 and 6 show the electrophoretic state of marker DNAs. Lane 2 shows the electrophoretic state of PCR product using DNA from cells cultured in the condition excluding IL-4, CD40L, TGF β or cycloheximide, as a template. Lane 3 shows the electrophoretic state of DNA product using DNA from cells cultured in the presence of cycloheximide only, as a template. Lane 4 shows the electrophoretic state of PCR product using DNA from cells cultured in the presence of IL-4, CD40L and TGF β , as a template. Lane 5 shows the electrophoretic state of PCR product cultured in the presence of IL-4, CD40L, TGF β , and cycloheximide, as a template.

[0193] Figure 1 (b) shows the result of Southern hybridization for DNA including an S α sequence looped out with class switch recombination, amplified by PCR using DNA derived from mouse B cell clone CH12F3-2 cultured under the various conditions.

[0194] Lane 1 shows the result of hybridization against PCR product using DNA from cells cultured in the condition excluding any of IL-4, CD40L, TGF β or cycloheximide, as a template. Lane 2 shows the result of Southern hybridization against PCR product using DNA from cells cultured in the presence of cycloheximide only, as a template. Lane 3 shows the result of hybridization against PCR product using DNA from cells cultured in the presence of IL-4, CD40L, and TGF β , as a template. Lane 4 shows the result of hybridization against PCR product using DNA from cells cultured in the presence of IL-4, CD40L, TGF β and cycloheximide, as a template.

[0195] Figure 2 is a photograph showing the production state of DNA including an S α sequence looped put with class switch recombination, amplified by PCR using DNA derived from mouse B cell clone CH12F3-2 cultured in various conditions.

[0196] Figure 2 (a) shows the electrophoretic state of DNA from DNA including an S α sequence looped out with

class switch recombination in mouse B cell clone CH12F3-2 cultured in the various conditions, stained with ethidium bromide.

[0197] Lanes 1 and 6 show the electrophoretic state of marker DNAs. Lane 2 shows electrophoretic state of PCR product using DNA from cells cultured in the condition excluding IL-4, CD40L, TGF β or cycloheximide, as a template. Lane 3 shows the electrophoretic state of DNA product using DNA from cells cultured in the presence of cycloheximide only, as a template. Lane 4 shows the electrophoretic state for PCR product using DNA from cells cultured in the presence of IL-4, CD40L and TGF β , as a template. Lane 5 shows the electrophoretic state for PCR product cultured in the presence of IL-4, CD40L, TGF β , and cycloheximide, as a template.

[0198] Figure 1 (b) shows the result of Southern hybridization for DNA including an S α sequence looped out with class switch recombination, amplified by PCR using DNA derived from mouse B cell clone CH12F3-2 cultured under the various conditions.

[0199] Lane 1 shows the result of hybridization against a PCR product using DNA from cells cultured under the condition excluding any one of IL-4, CD40L, TGF β or cycloheximide, as a template. Lane 2 shows the result of hybridization against a PCR product using DNA from cells cultured in the presence of cycloheximide only, as a template. Lane 3 shows the result of hybridization against a PCR product using the DNA from cells cultured in the presence of IL-4, CD40L, and TGF β , as a template. Lane 4 shows the result of hybridization against a PCR product using DNA from cells cultured in the presence of IL-4, CD40L, TGF β and cycloheximide, as a template.

[0200] Figure 3 shows the result of Northern blotting using a cDNA fragment coding a radiolabeled 23C9 (AID) protein, against mRNA derived from mouse B cell clone CH12F3-2 cultured under the various conditions.

[0201] Lane 1 shows the result of blotting against mRNA from cells cultured in the condition excluding any one of IL-4, CD40L, or TGF β or cycloheximide. Lane 2 shows the result of blotting against mRNA from cells cultured in the presence of cycloheximide, only. Lane 3 shows the result of blotting against mRNA from cells cultured in the presence of IL-4, CD40L and TGF β . Lane 4 shows the result of blotting against mRNA cultured in the presence of IL-4, CD40L, TGF β , and cycloheximide.

[0202] Figure 4 shows the result of Northern blotting using radio-labeled cDNA fragment coding 23C9 (AID) protein as a probe against mRNA derived from mouse B cell clone CH12F3-2 cultured in the various conditions.

[0203] Lane 1 shows the result of blotting against mRNA from cells cultured in the condition excluding IL-4, CD40L, TGF β or cycloheximide. Lane 2 shows the result of blotting against mRNA from cells cultured in the presence of cycloheximide, only. Lane 3 shows the result of the blotting against mRNA from cells cultured in the presence of IL-4, CD40L, and TGF β . Lane 4 shows the result of the blotting against mRNA from cells cultured in the presence of IL-4, CD40L, TGF β and cycloheximide.

[0204] Figure 5 shows the homology between an amino acid sequence of mouse AID protein and that of mouse APOBEC-1

[0205] An amino acid in a closed box shows an identical amino acid. A region in an open box indicates a cytidine deaminase motif. An amino acid with an asterisk (*) or an arrow indicates an amino acid conserved among APOBEC-1 proteins derived from rat, mouse, rabbit, and human.

[0206] Figure 6 shows a phylogenetic tree of various enzymes belonging to a cytosine nucleoside / nucleotide deaminase family, prepared based on cytidine deaminase motif.

[0207] Figure 7 shows a photograph indicating the electrophoretic state for AID-GST fusion protein in the molecular weight analysis by the gel electrophoresis and silver staining method.

[0208] Lane 1 shows the electrophoretic state for a marker molecule. Lane 2 shows the electrophoretic state for various proteins included in extracts from wild type *Escherichia coli* DH 5 α . Lane 3 shows the electrophoretic state for purified AID-GST fusion protein.

[0209] Figure 8 shows the electrophoretic state for AID-GST fusion protein by Western blotting using anti-AID protein peptide antibody.

[0210] Lane 1 shows the electrophoretic state for various proteins included in the extract from wild type *E. coli* DH5 α .

[0211] Lane 2 shows the electrophoretic state for purified AID-GST protein.

[0212] Figure 9 shows a cytidine deaminase activity depending on the concentrations of AID proteins.

[0213] Figure 10 shows the inhibitory effect of tetrahydouridine which is an inhibitor specific to cytidine deaminase on a cytidine deaminase activity in AID protein.

[0214] Figure 11 shows the inhibitory effect of each of 1,10-o-phenanthroline which is a zinc-chelating agent, and 1,7-o-phenanthroline which is an inactivated isomer thereof on a cytidine deaminase activity in AID protein.

[0215] Figure 12 is a photograph indicating expression state for mRNA of AID in various tissues in mouse, analyzed by Northern blotting method.

[0216] Figure 13 is a photograph indicating the expression state for mRNA of AID in various lymphatic tissues in mouse, analyzed by RT-PCR method.

[0217] Figure 14 is the photograph showing expression state for mRNA of AID as time goes, in activated mouse B cell clone CH12F3-2, analyzed by Northern blotting method.

[0218] Figure 15 a photograph showing expression state for mRNA of AID in mouse B cell clone CH12F3-2 stimulated with cytokine in various combinations, analyzed by Northern blotting.

[0219] Figure 16 shows a photograph indicating expression state for mRNA of AID in mouse spleen B cells, stimulated with stimulants in various combinations, analyzed by Northern hybridization method.

[0220] Figure 17 is a photograph indicating expression state for mRNA of AID in splenocytes derived from mice immunized with sheep red blood cells, analyzed by Northern blotting analysis.

[0221] Figure 18 shows expression state for mRNA of AID in splenocytes derived from mice immunized with sheep red blood cells, analyzed by RT-PCR.

[0222] Figure 19 is a photograph indicating localization of expression for AID mRNA in splenocytes derived from a normal mouse or a mouse immunized by sheep red blood cells, specifically, analyzed by in situ hybridization.

[0223] Figure 19 (A) and (D) indicate the result in the hybridization using a sense AID probe. Figure 19 (B) and (E) show localization for AID mRNA expression in hybridization using an antisense-AID probe. Figure 19 (C) and (F) show localization of germinal center in staining test by FITC-labeled PNA. Figures 19 (A) , (B) , and (C) indicate the result in the test using spleen tissues derived from normal mouse (before the immunization of sheep red blood cells). Figure 19 (D), (E), and (F) show the results of the examination using spleen tissue slices prepared 5 days after immunizing a mouse with sheep red blood cells.

[0224] Figure 20 is a photograph showing the localization of expression for AID mRNA in spleen tissue and payer's patch tissue, respectively, derived from a normal mouse or from a mouse immunized with sheep red blood cells, respectively, analyzed by in situ hybridization.

[0225] Figure 20 (A), (D), and (G) show the results in the hybridization using a sense AID probe. Figure 20 (B), (E), and (H) show the localization of the expression for AID mRNA in hybridization using an antisense AID probe. Figure 20 (C), (F), and (I) show the localization of germinating center in the staining test by FITC-labeled PNA. Figure 20 (A), (B), and (C) show the result of the examination using spleen tissues derived from a normal mouse (before immunization by sheep red blood cells). Figure 20 (D), (E), and (F) show the results of the examination using spleen tissue slices prepared 5 days after immunization of a mouse with sheep red blood cells. Figure 20 (G), (H), and (I) show the results of test using payer's patch prepared 5 days after the immunization of a mouse with sheep red blood cells.

[0226] Figure 21 schematically shows relative locations of partial nucleotide sequences of human genomic DNA coding human AID protein, which was amplified by PCR using various pairs of primers.

[0227] Figure 22 schematically shows a degree of homology between an amino acid sequence of mouse AID protein and that of human AID protein. The parts with a closed box are cytidine and deoxycytidylate deaminase zinc-binding region which is an AID protein active region.

[0228] Figure 23 schematically shows the structure of human genomic DNA including a gene coding human AID protein. One to five shows exon 1, exon 2, exon 3, exon 4, and exon 5, respectively.

[0229] Figure 24 is a photograph indicating the expression state for human AID mRNA in various types of human tissues, analyzed by RT-PCR.

[0230] Figure 25 is a photograph indicating a location (localization) of human AID gene on human chromosome, analyzed by Fluorescence in situ hybridization (FISH) method.

[0231] Two points at the tips of arrows show 12p13 where human AID gene exists.

Best Mode for Carrying out the Invention

[0232] The invention is illustrated in details by the following Examples, but not restricted to embodiments described in the Examples.

Example 1: Culture of for mouse B cell clone CH12F3-2 and confirmation of properties

[0233] Mouse B cell clone CH12F3-2 occurring class switch recombination (CSR) from IgM to IgA, several hours after the stimulation by IL-4, TGF- β , and CD40L, previously isolated by the present inventors, was cultured in the same manner as in the previous report (Immunity, Vol. 9, p. 1-10, 1998; Curr. Biol., Vol. 8, No. 4 p 227-230, 1998; Int. Immunol, Vol. 8, No. 2, p. 193-201, 1996).

[0234] When the CH12F3-2 is stimulated by IL-4, TGF- β , and CD40L, a circular DNA including an S region (switch region) looped out by class switch recombination was detected several hours after the stimulation.

[0235] The following manipulation was conducted according to the previous report (Curr. Biol., Vol. 8, No. 4, p. 227-230, 1998).

[0236] The B cell CH12F3-2 stimulated by IL-4, TGF- β , and CD40L, and that which was not stimulated were cultured for 6 hours in the presence or absence of cycloheximide (200 ng/ml) which is a protein synthesis inhibitor, respectively. Genomic DNA was extracted from each cell, and PCR was conducted with the DNA as a template by following the standard method to amplify circular DNA including an S μ sequence and an S α sequence. PCR was conducted by

using a pair of primers, α F1 and μ R3 and the other PCR was conducted by using a pair of primers, α F1 and μ R3.

[0237] As a control, genomic DNA coding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was amplified by PCR.

[0238] PCR product was subjected to the gel electrophoresis by ethidium bromide staining. Figure 1 (a) and Figure 2 show the results.

[0239] To confirm the presence or absence of the amplification of a circular DNA including the looped-out S region, Southern hybridization was conducted against the PCR product by using mouse α x region gene for a hybridization probe, according to the standard method (L. Sambrook E. F., Tom Maniatis., Second edition, Ed. Molecular Cloning (Nolan, C., Ed.) Cold Spring Harbor, 1989). As an α x gene, a 1,155 bp DNA fragment obtained by digesting 10 kb EcoRI cleaved fragment IgH703 with Hind III and Earl was used (Genbank #D11468, DNA No. 1993-3148) (J. Biol. Chem., Vol. 268, p. 4651-4665). Figures 1 (b) and 2 (b) show the results.

[0240] It has been shown that mouse B cell CH2F3-2 produces the looped-out DNA containing the α x sequence with the class switch recombination by the stimulation with cytokine, and the production of the DNA is inhibited by the presence of cycloheximide. This result suggested that occurrence of class switch recombination of an immunoglobulin gene needs a novel synthesis of a protein in the very early stage after the stimulation and the protein is deeply involved in the induction of the class switch.

Example 2: Identification of a gene which expression is improved in mouse B cell CH12F3-2 stimulated by cytokine

[0241] A gene which is presumably expressed in the early stage after mouse B cell clone CH12F3-2 is stimulated, and presumably play a role of introducing class switch recombination of an immunoglobulin gene was attempted to be isolate from the CH12F3-2 cells by the suppression subtract hybridization (SSH) (Proc. Natl. Acad. Sci. USA, Vol. 93, p. 6025-6030, 1996; Anal. Biochem., Vol. 240, p. 90-97, 1996) using the inhibitory PCR effect (Nucleic Acids Res., Vol. 23, p. 1087-1088, 1995).

[0242] A cDNA library necessary for subtraction cloning was prepared by using PCR-Select Subtraction Kit (CLON-TECH, Catalogue NO: K1804-1) by following the instruction manual supplemented with the kit in the experimental manipulation.

[0243] PolyA⁺RNA was isolated from each of mouse B cell clone CH12F3-2 stimulated with IL-4, TGF- β and CD40L for 5 hours, the same cells stimulated with the cytokines for 12 hours, and the cells which were not stimulated, by following the reported method (Nucleic Acids Res., Vol. 26, No. 4, p. 911-918, 1998) and treated with DNaseI to eliminate genomic DNA which may be mixed. Then cDNA was prepared based on each polyA⁺RNA sample using reverse transcriptase according to the standard method. Each cDNA prepared from mouse B cell clone CH12F3-2, treated with the above cytokines for 5 or 12 hours was mixed with same mole amounts to be used as a tester cDNA. On the other hand, cDNA derived from unstimulated cells was used as a driver cDNA.

[0244] Subtraction was conducted by adding the driver cDNA into the tester cDNA according to the above previous report and the experimental manipulation manual. The efficiency of subtraction was monitored by adding a small amount (1:1000 mole ratio) of ϕ X174 phage DNA cleaved at the restriction enzyme site Hae III, as a control, into the tester cDNA. After the subtraction, the phage DNA was concentrated to a mole ratio of about 100 times.

[0245] The subtracted cDNA was cloned to T-vector (Promega) according to the standard method to prepare a plasmid library. In the same manner as in the previous report, 2000 colonies in the library were screened by the differential hybridization method (Nucleic Acids Res., Vol. 26, No. 4, p. 911-918, 1998; Medical immunity, Vol. 29, No. Suppl. 17, p. 451-459, 1997). Each of the above tester cDNA and driver cDNA was radiolabeled to be used for hybridization. Clones including ϕ X174 phage DNA were selected by hybridizing ϕ X174 phage DNA with a replicant filter.

[0246] One hundred fifteen clones emitting a stronger signal than the radio-labeled driver cDNA probe against radio-labeled tester cDNA probe were identified and a nucleotide sequence of each clone was determined by using a DNA sequencer.

[0247] Northern blotting was conducted against mRNA obtained from mouse B cell clone CH12F3-2 stimulated with IL-4, TGF- β and CD40L or the same lines unstimulated, using the radio-labeled DNA inserted into the each clone as a probe, according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition, Ed. Molecular Cloning (Nolan, C., Ed.), Cold Spring Harbour, 1989). As a result, the enhanced expression corresponding to the stimulation with the above cytokines was observed in 23 among 115 clones. Gene fragments coding 7 different types of proteins, including genes coding the 3 kinds of known proteins and 4 kinds of novel proteins were found to be inserted into the 23 clones. Specifically, the expression of the 7 kinds of genes were found to be enhanced in mouse B cell clone CH12F3-2 by the stimulation with IL-4, TGF- β and CD40L.

<The known proteins>

[0248]

- 5 ABCD-1/MDC (8 clones)
- IFN γ receptor (2 clones)
- I-a (MHC class II) (1 clone)

< Novel proteins>

[0249]

- 23C9 (3 clones)
- 15B11 (7 clones)
- 15 8B9 (1 clone)
- 16A9 (1 clone)

[0250] As it has been known that the expression of the above I-a gene and ABCD/MDC gene is enhanced by stimulating mouse spleen B cell with IL-4 and CD40L, it was confirmed that the subtraction cloning was effectively conducted (J. Exp. Med., Vol. 188, No. 3, p. 451-463, 1998; Immunity, Vol. 5, No. 4. p. 319-330, 1996)

Example 3: Expression of mRNA for a novel protein 23C9 in mouse B cell clone CH12F3-2

[0251] The degree of enhanced expression of gene coding a novel protein 23C9 in mouse B cell clone CH12F3-2 stimulated with IL-4, TGF- β and CD40L was analyzed according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition, Ed. Molecular Cloning (Nolan, C., Ed.), Cold Spring Harbour, 1989) by Northern blotting.

[0252] Mouse B cell clone CH12F3-2 was cultured in the presence of one of the following reagents for 12 hours.

- (1) IL-4, TGF- β and CD40L only.
- (2) Cycloheximide which is a protein synthesis inhibitor (200 ng / ml), only
- (3) IL-4, TGF- β and CD40L as well as Cycloheximide (200 ng / ml)

[0253] Northern blotting was conducted against mRNA (10 μ g for each group) obtained in the same manner as the previous report (Nucleic Acid Res., Vol. 26, No. 4, p. 911-918, 1998) from each group of treated cells using a radio-labeled cDNA fragment (1,020 bp) coding a novel protein 23C9, obtained in the above Example, according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition, Ed. Molecular Cloning (Nolan, C., Ed.), Cold Spring Harbour, 1989).

[0254] As a control examination, Northern blotting was conducted for mRNA derived from B cell clone CH12F3-2 cultured without any one of the above cytokines, or cycloheximide.

[0255] The amount of mRNA to be electrophoresed was adjusted using the amount of mRNA in glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as an index. DNA amplified by RT-PCR using GF primer and GR primer was used as a probe for blotting of GAPDH mRNA (Location of nucleotides: 566-1016, Genbank U5299) (immunity, Vol. 9, P. 1-10, 1998).

[0256] Figures 3 and 4 show the results.

[0257] The expression of mRNA for a novel protein 23C9 was extremely strong in mouse B cell clone CH12F3-2 stimulated with IL-4, TGF- β and CD40L, while the expression in unstimulated cells was extremely weak. Expression of the mRNA in the stimulated cells was inhibited by the presence of a protein synthesis inhibitor. Moreover, in the stimulated cells, two bands indicating the expression of mRNA comprising different nucleotide lengths were detected.

[0258] Expression of mRNA for a novel protein 23C9 in each of the following mouse cell lines which do not originally comprise class switch recombination was examined by Northern blotting in the same manner as in the above.

[0259] B cell lines (IyD9, BA/F3, 70Z/3, WEHI231), T cell lines (EL-4, 2B4), myeloma cell lines (X63, HEHI-3). Fibroblast lines (L929, NIH3T3,) the other cell lines (F2, P815, ST2).

[0260] The expression of mRNA for the novel protein 23 C 9 was not observed in any cells.

Example 4: Cloning of a full length cDNA coding a novel protein 23C9.

[0261] Four different positive clones were obtained by screening cDNA library (Nucleic Acids Res., Vol. 26, No. 4, p. 911-918, 1998) prepared from mouse B cell clone CH12F3-2 stimulated with IL-4, TGF- β , and CD40L, using a cDNA

fragment (1,020 bp) coding the novel protein 23C9, obtained in the above Example as a probe. A nucleotide sequence of each clone was determined by using a DNA sequencer according to the standard method.

[0262] One clone comprises a 1.2 kb nucleotide length and a single reading frame (OPF) with 1 polyadenylation site. The other 3 clone comprise a 2.4 kb nucleotide length and 2 polyadenylation sites. A nucleotide sequence in the 1.2 kb part at the 5' side in the latter clones was identical to that of the nucleotides in the 1.2 kb DNA in the former (SEQ ID NO: 1).

[0263] Two different mRNA transcripts detected in Northern blotting in the above Example (Figures 3 and 4) were predicted to correspond to transcripts for each of the above 1.2kb and 2.4 kb, transcribed using the polyA site at 3' end and the polyA site at the 5'end.

[0264] A cDNA fragment coding the novel protein 23C9 used as a probe in the above (1,020 bp) was found to be a nucleotide sequence of from 847 to 1866 in the full length cDNA of 23C9.

[0265] A nucleotide sequence near a first initiation codon in each cDNA was fit to Kozak's rule (NucleicAcids Res., Vol. 15, No. 20, p. 8125-8148, 1987). In the 2.4kb cDNA, ATTTA which is a motif capable of mediating quick degradation of mRNA (Blood, Vol. 83, No. 11, p. 3182-3187, 1994) was present in the 2 sites in the untranslated region in the 3'side.

[0266] An open reading frame (ORF) of cDNA coding the novel protein 23C9 consisted of 198 amino acids with the expected molecular weight of about 24kDa (SEQ ID NO: 2). As a result of homology searching with known proteins by database, an amino acid sequence of ORF of the novel protein 23C9 comprised 34% amino acid homology with apolipoprotein B mRNA editing enzyme, catalytic polypeptide-1 (APOBEC-1) (Science, Vol. 260, No. 5115, p. 1816-1819, 1993, J. Biol. Chem., Vol. 268 No. 28, p. 20709-20712, 1993). GenBank and EMBL were used as DNA data base. SwissPlot was used as protein database. BLAST program (J. Mol. Biol., Vol. 215, No. 3, p. 403-410, 1990) and FASTA program (Proc. Natl. Acad. Sci. USA., Vol. 85, No. 8, p. 2444-2448 1988) were used for database search.

[0267] Figure 5 shows an amino acid sequence of ORF of the novel protein 23C9 and an alignment between the sequence and that of mouse APOBEC-1 amino acid sequence.

[0268] As a result of motif search on online using PROSITE (Nucleic Acids Res., Vol. 11 No. 20, p. 2013-2018, 1992), the APOBEC-1 like novel protein 23C9 comprises cytidine/deoxycytidine deaminase motif which is conserved in a amino acid sequence of a protein belonging to cytosine nucleoside/ nucleotide deaminase family which constructs a large family and is an activation site off a deaminase activity. A cytosine nucleoside/nucleotide deaminase family is classified into RNA editing deaminase, cytidine/deoxycytidylate deaminase, and CMP/dCMP deaminase based on the substrate specificity and homology in the activation sites (Cell, Vol. 81, No. 2, p. 187-195, 1995).

[0269] A phylogenic tree was prepared based on the alignment among regions in APOBEC-1 which is an RNA editing deaminase, cytosine nucleoside deaminase, cytosine nucleotide deaminase, and cytidine deaminase motif in the novel protein 23C9. The sequences in the known proteins used for the comparison were obtained from GenBank, as follows.

Human derived nucleoside deaminase: L27943
 Mouse derived nucleoside deaminase: AA388666
 S. subtilis derived nucleoside deaminase: U18532
 E. coli derived cytidine deaminase: X63144
 Rabbit derived APOBEC-1: U10695
 Human derived APOBEC-1: L25877
 Rat derived APOBEC-1: U10695
 Mouse derived APOBEC-1: U21951
 T2/T4 phage derived nucleotide deaminase: J05172
 Human derived nucleotide deaminase: L12136
 S. cerevisiae derived nucleotide deaminase: U10397

[0270] Figure 6 shows the result. Cytidine deaminase motif in the novel protein 23C9 was rather relative to a subgroup of RNA editing deaminase than subgroups of nucleoside deaminase and nucleotide deaminase.

[0271] On the other hand, a leucine-rich region existing at the C-terminus of APOBEC-1 is thought to be important for protein-protein interaction (Proc. Natl. Acad. Sci. USA., Vol. 91, No. 18, p. 8522-8526, 1994; J. Biol. Chem., Vol. 269, No. 34, p. 21725-21734, 1994). The novel protein 23C9 also comprised a leucine-rich region at the C-terminus. Four leucines in the region o 23C9 were conserved in the leucine rich regions of APOBEC-1 in rabbit, rat, mouse and human.

[0272] It has been known that Phe66, Phe87, His61, Glu63 and Cys93 are essential for binding of APOBEC-1 to RNA, and all these amino acid residues were conserved in the primary structure of 23C9 (Trends Genet., Vol. 12, No. 10 p. 418-424, 1996; Cell, Vol. 81, No. 2, p. 187-195, 1995, J. Biol. Chem., Vol. 270 No. 24, p. 14768-14775 1995; J. Biol. Chem., Vol. 270, No. 24, p. 14762-14767, 1995). From this fact, 23C9 protein is predicted to comprise an RNA editing deaminase activity.

[0273] Moreover, cytidine deaminase derived from APOBEC-1 and E. coli (ECCDA) are known to comprise a pseu-

doactive site domain at the C-terminus and the 23C9 protein also comprised a pseudoactive site domain same as in the APOBEC-1. This indicates that 23C9 protein is more relative to APOBEC-1 and ECCDA than deaminase proteins in the other groups.

[0274] From these facts, the novel protein 23C9 was named activation-induced cytidine deaminase (AID). The novel protein 23C9 was called AID hereafter.

Example 5: Preparation of the AID-GST fusion protein

[0275] The cDNA coding a full length AID cloned in the above Example was amplified by PCR with a pair of primers, AID-138 (SEQ ID NO: 3) and AID-161 (SEQ ID NO: 4), a pair of primers, AID-118 (SEQ ID NO: 5) and AID-119. (SEQ ID NO: 6) and Taq Polymerase by following the standard method. As there is an intron between AID-118 and AID-119, a PCR product derived from AID genomic DNA can be easily distinguished.

[0276] The obtained PCR product was subcloned to pGEX4T1 vector (Pharmacia) according to the standard method. A nucleotide sequence of the vector was determined and the absence of point mutation derived from the use of Taq polymerase in the full length AID cDNA cloned to the vector was confirmed.

[0277] *E. coli* DH5 α was transformed with the vector according to the standard method. The obtained transformants were cultured, and a full length AID cDNA was expressed as a fusion protein with glutathione S-transferase (GST). The AID-GST fusion protein was extracted in the same manner as in the previous report, and purified using glutathione agarose affinity chromatography (J. Biol. Chem., Vol. 270, No. 24, p. 14768-14775 1995).

[0278] A molecular weight of the purified AID-GST fusion protein was analyzed by following the standard method using 10% SDS-PAGE and silver staining. A protein extracted from wild type *E. coli* DH5 α was used as a control. Figure 7 shows the result.

[0279] As expected, the fusion protein was detected as a band comprising a molecular weight of about 49 kDa. Minor bands detected under the about 49 kDa were thought to be decomposed proteins, frequently generated in the purification process in general.

[0280] A molecular weight of the purified AID-GST fusion protein was analyzed by the Western blotting method according to the standard method (Genomics, Vol. 54, No. 1, p. 89-98, 1998). Anti-AID protein antibody to be used for the assay was prepared by immunizing a commercial rabbit for the experiment with multiple antigen peptides including synthetic peptides corresponding to amino acid NO: 116 to 132 of the AID protein of the present invention (Proc. Natl. Acad. Sci. USA., Vol. 85, No. 15, p. 5409, 1988).

[0281] Figure 8 shows the result.

Example 6: Cytidine deaminase activity of the AID protein

[0282] A cytidine deaminase activity of AID was measured by the same method as in the previous report (J Biol. Chem. Vol. 270, No. 24, p. 14768-14775, 1995).

[0283] The purified AID-GST fusion protein prepared in the above (2, 4, 6, 8, 10, 20, 40, 60, 100, 200, 300, 400, and 600 ng) was incubated in the buffer (pH 7.5, the total amount 10 μ l) containing 45mM Tris with 3.3 μ Ci [3 H] deoxycytidine (24.8 Ci / mmol, DuPont) and 250 μ M cytidine for 2 to 4 hours. The reaction was terminated by adding deoxycytidine (2 μ l of 10 μ g/ml) and deoxyuridine (2 μ l of 10 μ g/ml). Insoluble substances were removed by centrifugation, and the reaction mixture (4 μ l) was subjected to the polyethylene imine-cellulose thin layer chromatography plate (VWR). The plate was developed in isopropyl alcohol / 10% HCl (7:2 v/v). The plate was exposed to ultraviolet light (254 nm) for visualization and bands corresponding to deoxycytidine and deoxyuridine were collected, added to Ultima Gold scintillation solution to be quantified by liquid scintillation photometer (Packard)

[0284] Figure 9 shows the result. As a result, AID protein showed the cytidine deaminase activity depending on the concentrations.

[0285] An inhibitory effect of tetrahydrouridine (THU; 0 to 40 μ M) (Calbiochem, USA) which is an inhibitor specific to cytidine deaminase, on the cytidine deaminase activity in the AID-GST fusion protein (300 ng) was measured by the same method described above.

[0286] Figure 10 shows the result. The cytidine deaminase activity of AID protein was inhibited dependently on the concentrations of THU.

[0287] Each inhibitory effect of 1,10-o-phenanthroline (0 to 20 mM) which is a zinc-chelating agent and its inactive form isomer 1,7-o-phenanthroline (0 to 20 mM) on the cytidine deaminase activity in the AID-GST fusion protein was measured in the same manner as described below.

[0288] Figure 11 shows the result. The cytidine deaminase activity of AID protein was inhibited by 20 mM 1,10-o-phenanthroline by about 91%. 1,7-o-phenanthroline which is the inactive isomer only inhibited about 13%. These results indicate that AID protein is a zinc-dependent cytidine deaminase, same as APOBEC-1.

Example 7: Avidity of AID protein with AU-rich RNA

[0289] A recombinant APOBEC-1 binds to Au-rich RNA (Trends Genet., Vol. 12, No. 10, p. 418-424, 1996; Cell, Vol. 81, No. 2, p. 187-195, 1995; J. Biol. Chem., Vol. 270, No. 24, p. 14768-14775, 1995; J. Biol. Chem., Vol. 270, No. 24, p. 14762-14767, 1995), and progresses RNA editing for apoB in the presence of chicken extract including co-factor.

[0290] Since the AID protein has a functional cytidine deaminase activity as well as a structural similarity with APOBEC-1, to examine an RNA editing activity in the AID protein, avidity to AU-rich RNA (5-AU) and apoB RNA which are RNA substrate for APOBEC-1 was examined.

[0291] The AID protein did not show avidity to AU-rich RNA (5-AU) in the gel retardation assay. In *in vitro* apoB RNA assay, conversion from cytidine (C) to uridine (U) was not observed.

Example 8: Expression distribution of AID mRNA in tissues

[0292] The expression of AID mRNA in each tissue was examined by Northern blotting according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition, Ed. Molecular Cloning (Nolan C., Ed.), Cold Spring Harbour, 1989; Experimental Medicine, Suppl., "Genetic Engineering Hand Book", published by Yodosha, p. 133-140, 1992).

[0293] PolyA⁺RNA (2 µg each) obtained from cells derived from each tissue in mice (muscle, spleen, lung, heart, lymph node, brain, kidney, thymus, testis, liver) according to the previous report (Nucleic Acids Res., Vol. 26, No. 4, p. 911-918, 1998) was used as a sample. Radiolabeled cDNA fragment (1,020 bp) coding AID (23C9) obtained in the previous Examples was used as a probe for blotting polyA⁺RNA.

[0294] As a control, mRNA of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was blotted in the same manner. AS a probe for blotting GAPDH mRNA, DNA amplified by PCR using GP primer and GR primer was used. (Nucleotide location: 566-1016, Genbank, U52599) (Immunity, Vol. 9, p. 1-10, 1988).

[0295] Figure 12 shows the result.

[0296] As a result, AID mRNA was strongly expressed in mesenteric lymph node. In addition, weak expression was observed in spleen.

Example 9: Expression of AID mRNA in various lymphatic tissues.

[0297] The expression of AID mRNA in each lymphatic tissue was analyzed by RT-PCR according to the standard method (Immunity, Vol.9, p. 1-10, 1998).

[0298] cDNA was prepared according to the standard method using polyA⁺RNA obtained from cells derived from various lymphatic tissues (Payer's patch, mesenteric lymph node, axillary lymph node, spleen, bone marrow, thymus) in the same manner as in the previous report (Nucleic Acids Res., Vol. 26 No. 4, p. 911-918, 1998), for mRNA as a sample, as a template. AID cDNA and GAPDH cDNA were amplified using the obtained cDNA as a template. The pair of primers, AID-138 (SEQ ID NO: 3) and AID-161 (SEQ ID NO. 4) in the above, a pair of primers AID-118 (SEQ ID NO: 5) and AID-119 (SEQ ID NO: 6) and Taq polymerase were used for PCR of AID cDNA. As there is an intron between AID-118 and AID-119, a PCR product derived from the AID genomic DNA sequence can be easily distinguished.

[0299] Figure 13 shows the result.

[0300] AID cDNA was detected in all lymphatic tissues except for thymus. In particular, the obvious expression was observed in peripheral lymphatic organs, such as lymph node or Payer's patch. On the other hand, the expression in primary lymphatic organs was weak in comparison with that in the peripheral lymphatic organs.

Example 10: Expression of AID mRNA as time goes in activated mouse B cell clone CH12F3-2

[0301] Expression of AID mRNA as time goes in activated mouse B cell clone CH12F3-2 stimulated with IL-4 , TGF-β, and CD40L for 0 to 60 hours was analyzed by Northern blotting according to the standard method (L. Sambrook, E. F. , Tom Maniatis., Second edition Ed. Molecular Cloning (Nolan, C., Ed.). Cold Spring Harbor, 1989).

[0302] Mouse B cell clone CH12F3-2 was cultured in the presence of IL-4, TGF-β, and CD40L for the various periods (0, 3, 5, 12, 24, 36 48 or 60 hours).

[0303] Northern blotting was conducted against mRNA (10 µg in each group) obtained from each culture group in the same manner as in the previous report (Nucleic Acids Res., Vol. 26, No. 4 p. 911-918, 1998) using a radio-labeled cDNA fragment coding AID (23C9) obtained in the previous Examples, as a probe, according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition Ed. Molecular Cloning (Nolan, C., Ed.). Cold Spring Harbor, 1989).

[0304] The amount of mRNA to be gel-electrophoresed was adjusted by using mRNA of GAPDH as an index. DNA amplified by RT-PCR using GF primer and GR primer was used as a probe for blotting GAPDH mRNA (Nucleotide location: 566-1016, Genbank U52599) (Immunity, Vol. 9, p. 1-10, 1998).

[0305] Figure 14 shows the result.

[0306] It was shown that The expression of AID mRNA in mouse B cell clone CH12F3-2 was too small to be detected without the stimulation by cytokines, but that the expression was initiated 3 hours after the stimulation by cytokines (described in the above), was maximum 12 hours after the stimulation (more than about 15 times), and was gradually decreased from 48 hours after the stimulation.

Example 11: Cytokine specificity to inducing expression of AID mRNA in mouse B cell clone CH12F3-2.

[0307] Cytokine specificity to inducing expression of AID mRNA in mouse B cell clone CH12F3-2 was analyzed by Northern blotting according to the standard method L. Sambrook, E. F., Tom Maniatis., Second edition Ed. Molecular Cloning (Nolan, C., Ed.), Cold Spring Harbour, 1989).

[0308] Mouse B cell clone CH12F3-2 was cultured in the presence of various combinations of cytokines (one or more selected from IL-4 TGF- β , CD40-L) for 12 hours. Northern blotting was conducted against mRNA (10 μ g in each group) obtained from each culture group in the same manner as in the previous report (Nucleic Acids Res., Vol. 26, No. 4 p. 911-918, 1998) using a radio-labeled cDNA fragment (1,020 bp) coding AID (23C9) obtained in the previous Example, according to the standard method (L. Sambrook, E. F., TomManiatis., Second edition Ed. Molecular Cloning (Nolan, C., Ed.). Cold Spring Harbor, 1989).

[0309] The amount of mRNA to be gel-electrophoresed was adjusted by using mRNA of GAPDH as an index. DNA amplified by RT-PCR using GF primer and GR primer was used as a probe for blotting GAPDH mRNA (Nucleotide location: 566-1016, Genbank U52599) (Immunity, Vol. 9, p. 1-10, 1998).

[0310] Figure 15 shows the result.

[0311] Expression induction of AID-mRNA was small by solely any one kind of cytokines. On the other hand, when 3 kinds of cytokines described above were used at the same time, the maximum expression induction of AID-mRNA was observed.

[0312] As described in the above Example 3, because expression induction of AID mRNA was inhibited by cycloheximide which is an inhibitor for protein synthesis, it is hypothesized that enhanced expression of AID mRNA needs de nova synthesis.

Example 12: Expression induction of AID mRNA in spleen B cell by stimulation

[0313] The presence or absence of expression induction of AID mRNA by stimulation which may activate B cell and induce class switch recombination of immunoglobulin was examined.

[0314] Spleen B cell was purified and obtained from BALB/c mouse (6 to 12-week old, Shimizu Experimental Materials (SLC)) according to the standard method. Dead cells and cell fragments were removed by Ficoll density gradient centrifugation after the process of removing T cells. The purified spleen B cell was cultured for 4 days in the presence of a stimulus in various combinations (one or more selected from IL-4, TGF- β , CD40L and LPS (lipopolysaccharide) in the same manner as in the previous report (Nucleic Acids Res., Vol. 26, No. 4, p. 911-918, 1998). LPS derived from Salmonella typhosa (50 μ g/ml, Sigma) was used.

[0315] Northern blotting was conducted against mRNA (15 μ g in each group) obtained from each culture group in the same manner as in the previous report (Nucleic Acids Res., Vol. 26, No. 4 p. 911-918, 1998) using a radio-labeled cDNA fragment coding AID (23C9) obtained in the previous Example, according to the standard method (L. Sambrook, E. F., Tom Maniatis., Second edition Ed. Molecular Cloning (Nolan, C., Ed.). Cold Spring Harbor, 1989).

[0316] The amount of mRNA to be gel-electrophoresed was adjusted by using mRNA of GAPDH and 28S ribosomal RNA as an index. DNA amplified by RT-PCR using GF primer and GR primer was used as a probe for blotting GAPDHmRNA (Nucleotide location: 566-1016, Genbank U52599) (Immunity, vol. 9, p. 1-10, 1998).

[0317] Figure 16 shows the result.

[0318] The enhanced expression of AID mRNA by the stimulation with LPS only or LPS+IL-4, or LPS+TGF- β was observed in normal mouse spleen B cells.

Example 13: Induced expression of AID mRNA in vivo

[0319] It was examined whether the expression induction of AID mRNA by various stimulation in vitro would occur in vivo.

[0320] BALB/c mouse (6 to 12-week old, five individuals in each group, SLC) was immunized by intraperitoneally administering sheep red blood cell (SRBC) (1 X 10⁸ cells, Cosmo Bio.) . In the living body immunized by SRBC, it has been known that clonal expansion and germinal center formation occur after immunoresponse, and class switch recombination of an immunoglobulin gene and affinity maturation are caused.

[0321] PolyA*RNA was prepared from splenocytes isolated from spleen excised from each individual before (day 0) and after (day 2, 5, and 13) the immunization.

[0322] The PolyA⁺RNA (2 µg each) was subjected to the Northern blotting using the radiolabeled cDNA fragment (1,020 bp) coding AID (23C9) as a probe in the same manner as the above Examples. The amount of mRNA to be gel-electrophoresed was adjusted using mRNA of GAPDH as an index in the same manner as in the above Examples.

[0323] Figure 17 shows the result.

[0324] The minimum amount of expressed AID mRNA was detected before immunization of SRBC (day 0), however, a significant enhancement of expression (about 4 to 5 times) was observed day 5 and day 13 after the immunization.

[0325] Moreover, to analyze in which cell type enhanced expression of AID mRNA occurs, RT-PCR was conducted by the standard method (Immunity, Vol. 9, p. 1-10, 1998).

[0326] Red blood cells were removed from splenocytes obtained from spleen which was obtained 5 days after the immunization of SRBC in the same manner as the above, and T cells and non-T cells were separated using nylon fiber (Wako Pure Chemicals) in the same manner as in the previous report (Eur. J. Immunol., Vol. 3, No. 10, p. 645-649, 1973). T cell fraction contained more than 90% of CD3 positive cells, and less than 20% B 220 positive cells. T-cell fraction (removal of B cells) and B-cell fraction were concentrated by MACS method with magnetic beads conjugated to anti-CD19 antibody (Miltenyi Biotech.). B220 positive B cells included in the fraction in which T cells were removed were 5% or less. On the other hand, B220 positive B cells included in the fraction in which CD19 positive cells were concentrated were 60% or more.

[0327] cDNA was prepared by reverse transcriptase according to the standard method using polyA⁺RNA prepared from each fractionated cell group. AID cDNA and GAPDH cDNA were amplified by PCR using the obtained cDNA as a template. For PCR of AID cDNA, the previously described pair of primers, AID-138 (SEQ ID NO: 3) and AID-161 (SEQ ID NO: 4), and the previously described pair of primers, AID-118 (SEQ ID NO: 5) and AID-119 (SEQ ID NO: 6), as well as Taq polymerase were used.

[0328] Figure 18 shows the result.

[0329] As a result, in the CD19 positive B cell fraction and non-T cell fraction, amplification of AID cDNA was observed. Specifically, it was demonstrated that enhanced expression of AID mRNA induced by immunization by SRBC occurs in spleen CD19 positive B cells.

Example 14: Localization of AID mRNA expression in lymphatic organs

[0330] It was found that timing of enhanced expression of AID mRNA in spleen almost consistent with the initiation of germinal center (GC) formation after immunization of SRBC, from the result of the previous Examples. In this examination, an precise localization of AID mRNA expression in lymphatic organs was analyzed using in situ hybridization.

[0331] AID cDNA cleaved out by digesting pGEX4T1 vector in which cDNA coding AID protein has been subcloned, with EcoRI and XhoI was subcloned into plasmid pBluescriptSK (+) (Stratagene). The plasmid was digested with EcoRI or XhoI to obtain linearized plasmid DNA and transcribed into RNA using the plasmid as a template in the presence of digoxigenin-labeled rUTP (Boehringer-Mannheim) using T3 RNA polymerase or T7 RNA polymerase to prepare each of digoxigenin-labeled antisense probe and sense probe.

[0332] On the other hand, frozen tissue slices were prepared by immobilizing with paraformaldehyde from each of spleen and payer's patch in a normal mouse as a lymphatic organ sample. A normal mouse was immunized with SRBC in the same manner as in the above Examples, and frozen tissue slices immobilized with paraformaldehyde from spleen obtained 5 day after the immunization.

[0333] Hybridization was conducted by applying the digoxigenin-labeled antisense AID probe or sense AID probe to each of the slides furnished with each of immobilized slices. Hybridized digoxigenin-labeled AID probe was detected using anti-digoxigenin antibody conjugated with alkaline phosphatase. The localization of anti-digoxigenin antibody conjugated to digoxigenin on the probe was identified by detecting a phosphatase reactant (dark purple color). This analysis was conducted using a light transmission microscope.

[0334] In situ hybridization and detection of riboprobe in this examination were conducted in the same manner as in the previous report (J. Comp. Neurol., Vol. 333, No. 3, p. 398-416, 1993).

[0335] The location of germinal center in each tissue slice was identified by staining with PNA (Vector) conjugate with FITC and observing with a inflorescent microscope.

[0336] Figures 19 and 20 show the result.

[0337] In the examination using the antisense AID probe, multiple obvious focal signals were observed in spleen tissue slices derived from SRBC immunized mouse (day 5 after the immunization) (Figure 19 (E) and 20 (E)), however, any signals were not detected in spleen tissue slices derived from mice which were not immunized with SRBC (Figure 19 (B) and 20 (B)). This result is consistent with the result of Northern blotting obtained in the above Example (Figure 17). Existence of germinal center was observed both in spleen tissue slices derived from SRBC-immunized mouse (day 5 after the immunization) (Figures 19 (F) and 20 (F)) as well as in the normal payer's patch (Figure 20 (I)) , by staining with FITC-labeled PNA. The expression of AID mRNA was found to localize in germinal center in the both tissue slices .

[0338] In the examination using sense AID probe, any signals as background were not detected in tissue slices of spleen or of Peyer's patch regardless of presence or absence of the immunization by SRBC.

[0339] This result indicates that expression induction of AID mRNA occurs in specifically to germinal center B cells, activated by stimulation with an antigen.

Example 15: Isolation of genomic DNA coding AID protein derived from human

<15-1> Preparation of probes for hybridization

[0340] PCR was conducted using an expression vector prepared by inserting cDNA coding a full length mouse AID protein, prepared in Example 5 into a plasmid vector pGEX4T1, as a template with a pair of primers (Primer 170: SEQ ID NO: 16 and primer 181: SEQ ID NO: 179, according to the standard method described in the above.

[0341] The obtained PCR product was purified by the standard method described above and a nucleotide sequence of the purified DNA was determined by the direct sequence method to confirm that the purified DNA is the nucleotide sequence coding a full length of mouse AID protein. This purified DNA was used as a probe for hybridization in the following experiments.

<15-2> Screening of human genomic DNA library

[0342] The probe prepared in the above was labeled in the same manner as for the radioactive probe in the above Northern hybridization to make a probe radio-labeled by a radioactive isomer.

[0343] Using the labeled probe, a commercial human genomic DNA library (catalogue No. HL1067j; Lot No. 45003; CLONTECH) was screened by the cross hybridization according to the standard method.

[0344] Washing after the hybridization was conducted twice in 2 X SSC (including 0.1% SDS, under the room temperature, 10 min), and twice in 2 X SSC (including 0.1% SDS, 65°C, 30 min). Phage DNA was subcloned by purifying phage DNA and inserting about 22 kb genomic DNA obtained by cleaving at NotI restriction enzyme site in the phage DNA, into NotI restriction enzyme site in plasmid pZero-2.1. This plasmid was named 3CpZero.

[0345] A DNA fragment obtained by digesting 3CpZero with PstI was ligated to the PstI site of plasmid pBlueScript KS (Toyobo) and E. coli was transformed with this ligated DNA.

[0346] Transformants were screened by the colony hybridization using the labeled probe prepared in the above according to the standard method, and multiple positive clones were obtained.

[0347] A nucleotide sequence of human genomic DNA inserted into each positive clone was analyzed and multiple clones containing genomic DNA of DNA coding human AID protein were identified.

[0348] Among the multiple clones, nucleotide sequences of genomic DNA containing DNA coding human AID protein contained in two clones were described in SEQ ID NOs: 9 and 10, respectively.

[0349] Moreover, a nucleotide sequence of genomic DNA including DNA coding human AID protein included in the positive other clone was shown in SEQ ID No: 35.

Example 16: Isolation of cDNA coding a full-length human AID protein and preparation of human AID protein

[0350] By comparing a nucleotide sequence of genomic DNA including a coding region of the obtained human AID protein with cDNA nucleotide sequence coding a full-length mouse AID protein determined in the above, a human AID protein coding region in the human genomic DNA was deduced.

[0351] A pair of primers for RACE-PCR was designed based on the deduced nucleotide sequence of the coding region in the human AID protein (Primer 22: SEQ ID NO: 18, and primer 25: SEQ ID NO: 19).

[0352] RACE-PCR was conducted using mRNA prepared from human B Lymphoma cell line RAMOS as a template with the above pair of primers according to the previous report (J. Biol. Chem., Vol. 274, p. 18470-18476, 1999) by following the standard method. A nucleotide sequence of the obtained PCR product was determined and cDNA coding a full length human AID protein was obtained (cDNA sequence: SEQ ID NO: 7, and amino acid sequence: SEQ ID 8).

[0353] As a result, human AID protein (SEQ ID NO: 8) has extremely high homology in amino acid sequences with a mouse AID protein (SEQ ID NO: 2) (Figure 22). Amino acid sequences in Cytidine and deoxycytidilate deaminase zinc-binding region which is an active region in AID protein (both mouse AID and human AID SEQ ID NO: 56 to 94) were completely consistent (conserved) between mouse and human.

[0354] As a partial amino acid sequence (amino acid NO: 116 to 132 in SEQ ID NO: 2) of mouse AID protein used for the preparation of anti-AID protein antibody (Example 5) was completely consistent with a corresponding amino acid sequence (amino acid NO: 116 to 132 in SEQ ID NO: 8) of human AID protein, the anti-AID protein antibody was expected to comprise cross-reactivity not only with mouse AID protein but also with human AID protein.

[0355] Human AID cDNA obtained in the above was reconstructed according to the standard method in the manner

of genetic engineering so that His-AID fusion protein added with His-tag (a peptide of histidine repeated 10 times) at N-terminal in the human AID protein was produced, and an expression vector was prepared by inserting the cDNA into a plasmid pEF-BOS (Unexamined published Japanese patent No. Hei 2-242687). The vector was introduced into monkey kidney derived cell line COS7 by lipofection using LIPOFECTAMINE (GIBCO BRL) according to the standard method. The obtained transgenic cells were cultured by the standard method and His-human AID fusion protein was transiently expressed. His-human AID fusion protein was extracted and purified in the same method as the previous report, and the production of His-human AID fusion protein was analyzed by Western blotting with the anti-AID antibody prepared in Example 5 and a commercial anti-His tag antibody according to the standard method. As a result, the His-AID protein was detected as a band comprising about 31 kDa molecular weight in all cases using any antibody.

Example 17: Determination of exons in genomic DNA coding human AID protein

[0356] Based on the information for the nucleotide sequence of cDNA coding the full length human AID protein above, exons in the nucleotide sequences for genomic DNA coding human AID protein in the above were determined.

[0357] As a result, it was confirmed to consist of 5 exons.

Exon 1 (Nucleotide sequence: SEQ ID NO: 11);
 Exon 2 (Nucleotide sequence: SEQ ID NO: 12);
 Exon 3 (Nucleotide sequence: SEQ ID NO: 13);
 Exon 4 (Nucleotide sequence: SEQ ID NO: 14); and
 Exon 5 (Nucleotide sequence: SEQ ID NO: 15).

[0358] The exon 1 contains a translation initiation codon ATG which codes the first methionine (Amino acid No: 1 of SEQ ID NO: 8) in human AID protein, and the initiation codon corresponds to nucleotide NOs: 80 to 82 in SEQ NO: 11.

[0359] Specifically, the genomic DNA including DNA coding human AID obtained in the above Examples (SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 35) consists of introns and exons described below and comprises a full length of about 11 kb. Figure 23 schematically shows the structure.

<SEQ ID NO: 9>

[0360]

Intron: Nucleotide NOs: from 1 to 1031
 Exon 1: Nucleotide NOs: from 1032 to 1118
 Intron: Nucleotide NOs: from 1119 to 5514

<SEQ ID NO: 10>

[0361]

Intron: Nucleotide NOs: from 1 to 1064
 Exon 2: Nucleotide NOs: from 1065 to 1212
 Intron: Nucleotide NOs: from 1213 to 2591
 Exon 3: Nucleotide NOs: from 2592 to 2862
 Intron: Nucleotide NOs: from 2863 to 3155
 Exon 4: Nucleotide NOs: from 3156 to 3271
 Intron: Nucleotide NOs: from 3272 to 3740
 Exon 5: Nucleotide NOs: from 3741 to 5912
 Intron: Nucleotide NOs: from 5913 to 6564

<SEQ ID NO: 35>

[0362]

Intron: Nucleotide NOs: from 1 to 441
 Exon 1: Nucleotide NOs: from 442 to 528
 Intron: Nucleotide NOs: from 529 to 6279
 Exon 2: Nucleotide NOs: from 6280 to 6427

Intron: Nucleotide NOs: from 6428 to 7806
 Exon 3: Nucleotide NOs: from 7807 to 8077
 Intron: Nucleotide NOs: from 8078 to 8370
 Exon 4: Nucleotide NOs: from 8371 to 8486
 Intron: Nucleotide NOs: from 8487 to 8955
 Exon 5: Nucleotide NOs: from 8956 to 11067
 Intron: Nucleotide NOs: from 11068 to 11204

Example 18: Amplification of a given partial nucleotide sequence of genomic DNA coding human AID protein by PCR and diagnosis for the presence or absence of mutation in the partial nucleotide sequence

[0363] The AID protein of the present invention may involve in sideration of various immunodeficiency and allergic disease. For example, a given immunodeficiency or allergic disease may be caused by mutation or deletion in the nucleotide sequence of genomic DNA (especially exon) coding an AID protein.

[0364] The presence or absence of such mutation or deletion in genomic DNA can be analyzed by, for example, following examples.

(1) A pair of primers comprising a nucleotide sequence complementary to a given partial nucleotide sequence of genomic DNA coding AID protein in the present invention is prepared.

(2) Using genomic DNA coding AID protein obtained from tissues or cells of a patient suffering from immunodeficiency or allergic disease as a template, an objective partial nucleotide sequence of the genomic DNA is amplified with the pair of primer DNA.

(3) By analyzing the presence or absence of a PCR product and a nucleotide sequence of the PCR product, and comparing the nucleotide sequence with a corresponding nucleotide sequence in genomic DNA coding AID protein derived from a normal person, mutation or deletion in the genomic DNA is identified.

[0365] Specifically, this method enables, for example, not only elucidate relationship between immunodeficiency or allergic disease and AID protein, but also diagnose the diseases by the above method in the case that AID protein is a cause of sideration of a given type of disease (for example immunodeficiency or allergic disease).

[0366] For the above purpose, the following 15 kinds of primers were designed and prepared based on a given partial nucleotide sequence in the genomic DNA coding human AID protein.

Primer: p3 (SEQ ID No. 20)
 Primer: p9 (SEQ ID No. 21)
 Primer: p10 (SEQ ID No. 22)
 Primer: p12 (SEQ ID No. 23)
 Primer: p14 (SEQ ID No. 24)
 Primer: p16 (SEQ ID No. 25)
 Primer: p17 (SEQ ID No. 26)
 Primer: p19 (SEQ ID No. 27)
 Primer: p26 (SEQ ID No. 28)
 Primer: p29 (SEQ ID No. 29)
 Primer: p36 (SEQ ID No. 30)
 Primer: p48 (SEQ ID No. 31)
 Primer: p59 (SEQ ID No. 32)
 Primer: p85 (SEQ ID No. 33)
 Primer: p86 (SEQ ID No. 34)

[0367] By PCR using the above primers as a pair of primers by the following combinations, and a genomic DNA isolated from human B lymphoma cell RAMOS as a template, a partial nucleotide sequence coding each target human AID protein was amplified. Figure 21 shows relative locations of genomic DNA partial nucleotide sequences amplified by each primer pair.

(1) DNA comprising nucleotide sequence of SEQ ID NO: 31 and DNA comprising nucleotide sequence of SEQ ID NO: 32;

(2) DNA comprising nucleotide sequence of SEQ ID NO: 20 and DNA comprising nucleotide sequence of SEQ ID NO: 22;

(3) DNA comprising nucleotide sequence of SEQ ID NO: 21 and DNA comprising nucleotide sequence of SEQ ID

NO: 30;
 (4) DNA comprising nucleotide sequence of SEQ ID NO: 24 and DNA comprising nucleotide sequence of SEQ ID NO: 25;
 (5) DNA comprising nucleotide sequence of SEQ ID NO: 23 and DNA comprising nucleotide sequence of SEQ ID NO: 27;
 (6) DNA comprising nucleotide sequence of SEQ ID NO: 23 and DNA comprising nucleotide sequence of SEQ ID NO: 28;
 (7) DNA comprising nucleotide sequence of SEQ ID NO: 23 and DNA comprising nucleotide sequence of SEQ ID NO: 29;
 (8) DNA comprising nucleotide sequence of SEQ ID NO: 26 and DNA comprising nucleotide sequence of SEQ ID NO: 27;
 (9) DNA comprising nucleotide sequence of SEQ ID NO: 26 and DNA comprising nucleotide sequence of SEQ ID NO: 28;
 (10) DNA comprising nucleotide sequence of SEQ ID NO: 26 and DNA comprising nucleotide sequence of SEQ ID NO: 29;
 (11) DNA comprising nucleotide sequence of SEQ ID NO: 34 and DNA comprising nucleotide sequence of SEQ ID NO: 28;
 (12) DNA comprising nucleotide sequence of SEQ ID NO: 34 and DNA comprising nucleotide sequence of SEQ ID NO: 29;
 (13) DNA comprising nucleotide sequence of SEQ ID NO: 33 and DNA comprising nucleotide sequence of SEQ ID NO: 29; or,
 (14) DNA comprising nucleotide sequence of SEQ ID NO: 18 and DNA comprising nucleotide sequence of SEQ ID NO: 19;

[0368] The condition for PCR was set by the following manner.

<Reaction solution>

[0369] A total amount of 20.2 µl consisting of DDW (8 µl), 10 X buffer (2 µl), dNTP (2.5 mM each, 2 µl), 2 µM primer 1 (2 µl), 2 µM primer 2 (2 µl), genomic DNA isolated from human B Lymphoma cells (185 ng/µl) and Taq polymerase (5U/ml, 0.2 µl), Ex Taq (TAKARA), or Ampli Taq (Perkin Elmer)

< Reaction>

[0370] Reaction was conducted by the following (A) or (B).

(A) 1 cycle (reaction at 94°C for 30 sec) and 40 cycles (reaction at 94 °C for 10 sec, reaction at 54 °C for 30 sec, and reaction at 72 °C for 3 min and 30 sec) and stored at 4 °C

(B) 1 cycle (reaction at 94 °C for 30 sec) and 40 cycles (reaction at 94 °C for 10 sec, reaction at 55 °C for 30 sec, and reaction at 72 °C for 2 min and 10 sec) and stored at 4 °C.

< PCR equipment>

[0371] A commercial PCR device (Perkin Elmer Thermal Cycler 9700 type) was used.

Example 19: The expression of human AID mRNA in various human organ tissues

[0372] The expression of human AID mRNA in various human organ tissues was analyzed by RT-PCR according to the standard method (Immunity, Vol. 9, p. 1-10, 1998).

[0373] RT-PCR was conducted by using various tissues set in the human tissue cDNA panel (CLONTECH) as a template according to the standard method.

[0374] AID cDNA was amplified by primers p17 (SEQ ID NO: 26) and p26 (SEQ ID NO: 28) prepared in the above and Taq polymerase.

[0375] As a control, RT-PCR in the same manner was conducted using cDNA of G3PDH as a template and GF primer and GR primer (Immunity, Vol. 9, p.1-10, 1998).

[0376] Figure 24 shows the result. As a result, Specific expression of mRNA was confirmed in lymph node and tonsil. This result was consistent with the experimental result in which the expression of mRNA for mouse AID was observed in the various lymphatic tissues (Examples 8 and 9).

[0377] On the other hand, when RT-PCR was conducted with the saturated cycle number in the same manner as the above in the above RT-PCR, the expression of AID mRNA was observed in almost all analyzed organs .

Example 20: Localization of human AID gene on human chromosomes

[0378] Localization of human AID gene on human chromosomes was analyzed by Fluorescence in situ hybridization (FISH) method (Experimental Medicine, Suppl. "Genetic Engineering Hand Book" published by Yodosha, 1992, p. 271-277).

[0379] Genomic DNA including human AID gene (exon 1 to exon 5), isolated in the above, which was labeled with biotin-11-dUTP (Sigma) by the nick translation method was used as a probe for hybridization.

[0380] The probe was hybridized with chromosomes in metaphase human cells. Hybridization signals were detected using fluorescein isothiocyanate-avidin (DCS) (Vector Laboratories).

[0381] Figure 25 shows the result. As a result, human AID gene was found to be localized on chromosome 12p13. Moreover, this location was revealed to be near 12p13.1 which is the location for the above APOBEC-1 comprising a relatively high amino acid sequence homology with the AID protein and has the same cytidine deaminase activity as that of the AID protein.

[0382] It has been reported that some abnormality on human chromosome locus 12p13.3-12p11.2, 12p13.2-12p24.1 and 12p13 may be involved in diseases such as acrocallosal syndrome, inflammatory bowel syndrome familial periodic fever, respectively, however, causative gene thereof has not been traced yet. It has been suggested that human AID gene of the present invention may be involved in sideration of such diseases .

Industrial Applicability

[0383] The AID protein of the present invention can be considered to have a function of regulating various biological mechanisms required for generation of antigen-specific immunoglobulins (specific antibodies), which eliminate non-self antigen (foreign antigen, self-reacting cells, etc.) that triggers various diseases. More specifically, the AID protein of the present invention can be considered to be one of the enzyme that plays an important role in the genetic editing such as RNA editing and so on occurring in germinal center B cells, such as activation of B cells, class switch recombination of immunoglobulin gene, somatic hypermutation, and affinity maturation, which are the mechanisms for generation of immunoglobulin having high specificity to antigens.

[0384] The dysfunction of the AID protein of the present invention can be the cause for the humoral immunodeficiency since it induces failure of germinal center B cell function, such as antigen-specific B cell activation, class switch recombination, and somatic mutation. Reversely, the breakdown of the regulation of AID protein may induce allergy disease or autoimmune disease since it can cause inappropriate B cell activation and needless class switch recombination and somatic mutation.

[0385] Therefore, regulation of the function of AID protein and the gene encoding it enables preventing and treating various immunodeficiencies, autoimmune diseases , and allergies , which result from, for example, B cell dysfunctions (e.g. IgA deficiency, IgA nephropathy, γ globulinemia, hyper IgM syndrome, etc.) or class switch deficiency of immunoglobulin. Thus, the AID protein and the gene encoding the AID protein can be targets for the development of drugs for therapy of diseases mentioned above.

[0386] Examples of diseases whose onset prevention, symptom remission, therapy and/or symptomatic treatment effect is expected by regulating the function of the AID protein of the present invention or the gene encoding it include, for example, primary immunodeficiency syndrome with congenital disorder of immune system, mainly immunodeficiency considered to develop by B cell deficiency, decrease, or dysfunction (e.g. sex-linked agammaglobulinemia, sex-linked agammaglobulinemia with growth hormone deficiency, immunoglobulin deficiency with high IgM level, selective IgM deficiency, selective IgE deficiency, immunoglobulin heavy chain gene deletion, κ chain deficiency, IgA deficiency, IgG subclass selective deficiency, CVID (common variable immunodeficiency), infantile transient dysgammaglobulinemia, Rosen syndrome, severe combined immunodeficiency (sex-linked, autosomal recessive), ADA (adenosine deaminase) deficiency, PNP (purine nucleoside phosphorylase) deficiency, MHC class II deficiency, reticular dysplasia, Wiskott-Aldrich syndrome, ataxia telangiectasia, DiGeorge syndrome, chromosomal aberration, familial Ig hypermetabolism, hyper IgE syndrome, Gitlin syndrome, Nezelof syndrome, Good syndrome, osteodystrophy, transcobalamin syndrome, secretory bead syndrome, etc.), various diseases with antibody production deficiency that are secondary immunodeficiency syndrome with disorder of immune system caused by an acquired etiology (for example, AIDS, etc.), and/or various allergic diseases (e.g., bronchial asthma, atopic dermatitis, conjunctivitis, allergic rhinitis, allergic enteritis, drug-induced allergy, food allergy, allergic urticaria, glomerulonephritis, etc.). These could be targets for drug development.

[0387] Namely, the AID protein of the present invention, a fragment thereof, a DNA encoding the AID protein, a fragment thereof, and an antibody against the AID protein are useful as reagents for developing drugs for prevention

and therapy of such diseases.

[0388] Also, the DNA itself is useful as an antisense drug regulating the function of AID gene at a gene level and in a use in gene therapy. The protein or the fragments thereof (e.g. enzyme active site) itself is useful as a drug.

[0389] Furthermore, an antibody reactive to the AID protein of the present invention or a fragment thereof is extremely useful as an antibody drug by regulating functions of the AID protein.

[0390] Furthermore, the gene (DNA) , protein, and antibody of the present invention are useful as reagents for searching substrates (e.g. RNA, etc.) interacting (binding) with the protein (enzyme) of the present invention, or other auxiliary proteins associated with the protein of the present invention, and for developing drugs targeting the substrates and auxiliary proteins.

[0391] Furthermore, a method for identifying a substance that regulates production of the AID protein of the present invention or transcription of a gene encoding the AID protein into mRNA are extremely useful as means to develop drugs for therapy and prevention of various diseases (especially, immunodeficiency and allergic disease) in which the above-mentioned AID protein or AID gene is considered to be involved.

SEQUENCE LISTING

5

<110> Japan Tobacco, Inc.

Honjo, Tasuku

10

<120> Novel Cytidine Deaminase

15

<130> J1-101DP2PCT

20

<140>

<141>

25

<150> JP11-087192

<151> 1999-03-29

30

<150> JP11-178999

<151> 1999-06-24

35

<150> JP11-371382

<151> 1999-12-27

40

45

<160> 35

50

<170> PatentIn Ver. 2.1

55

<210> 1

<211> 2440

5

<212> DNA

<213> *Mus musculus*

10

<220>

<221> CDS

15

<222> (93).. (689)

20

<220>

<221> 5' UTR

<222> (1).. (92)

25

<220>

30

<221> 3' UTR

<222> (690).. (2440)

35

<400> 1

ggcacgagca gcactgaagc agccttgctt gaagcaagct tcctttggcc taagacttg 60

40

agggagtcaa gaaagtcacg ctggagaccg at atg gac agc ctt ctg atg aag 113

45

Met Asp Ser Leu Leu Met Lys

1

5

50

caa aag aag ttt ctt tac cat ttc aaa aat gtc cgc tgg gcc aag gga 161

Gln Lys Lys Phe Leu Tyr His Phe Lys Asn Val Arg Trp Ala Lys Gly

55

10

15

20

5 cgg cat gag acc tac ctc tgc tac gtg gtg aag agg aga gat agt gcc 209
 Arg His Glu Thr Tyr Leu Cys Tyr Val Val Lys Arg Arg Asp Ser Ala
 25 30 35

10 acc tcc tgc tca ctg gac ttc ggc cac ctt cgc aac aag tct ggc tgc 257
 Thr Ser Cys Ser Leu Asp Phe Gly His Leu Arg Asn Lys Ser Gly Cys
 15 40 45 50 55

20 cac gtg gaa ttg ttg ttc cta cgc tac atc tca gac tgg gac ctg gac 305
 His Val Glu Leu Leu Phe Leu Arg Tyr Ile Ser Asp Trp Asp Leu Asp
 25 60 65 70

30 ccg ggc cgg tgt tac cgc gtc acc tgg ttc acc tcc tgg agc ccg tgc 353
 Pro Gly Arg Cys Tyr Arg Val Thr Trp Phe Thr Ser Trp Ser Pro Cys
 75 80 85

35 tat gac tgt gcc cgg cac gtg gct gag ttt ctg aga tgg aac cct aac 401
 40 Tyr Asp Cys Ala Arg His Val Ala Glu Phe Leu Arg Trp Asn Pro Asn
 90 95 100

45 ctc agc ctg agg att ttc acc gcg cgc ctc tac ttc tgt gaa gac cgc 449
 Leu Ser Leu Arg Ile Phe Thr Ala Arg Leu Tyr Phe Cys Glu Asp Arg
 50 105 110 115

55 aag gct gag cct gag ggg ctg cgg aga ctg cac cgc gct ggg gtc cag 497

EP 1 174 509 A1

Lys Ala Glu Pro Glu Gly Leu Arg Arg Leu His Arg Ala Gly Val Gln
 120 125 130 135
 5
 atc ggg atc atg acc ttc aaa gac tat ttt tac tgc tgg aat aca ttt 545
 10
 Ile Gly Ile Met Thr Phe Lys Asp Tyr Phe Tyr Cys Trp Asn Thr Phe
 140 145 150
 15
 gta gaa aat cgt gaa aga act ttc aaa gcc tgg gaa ggg cta cat gaa 593
 20
 Val Glu Asn Arg Glu Arg Thr Phe Lys Ala Trp Glu Gly Leu His Glu
 155 160 165
 25
 aat tct gtc cgg cta acc aga caa ctt cgg cgc atc ctt ttg ccc ttg 641
 30
 Asn Ser Val Arg Leu Thr Arg Gln Leu Arg Arg Ile Leu Leu Pro Leu
 170 175 180
 35
 tac gaa gtc gat gac ttg cga gat gca ttt cgt atg ttg gga ttt tga 689
 40
 Tyr Glu Val Asp Asp Leu Arg Asp Ala Phe Arg Met Leu Gly Phe
 185 190 195
 45
 aagcaacctc ctggaatgac acacgtgatg aaatttctct gaagagactg gatagaaaaa 749
 50
 caacccttca actacatggt tttcttctta agtactcact tttataagt tagggggaaa 809
 55
 ttatatgact ttttaaaaaa tacttgagct gcacaggacc gccagagcaa tgatgtaact 869
 gagcttgctg tgcaacatcg ccactactg gggaacagca taacttccag actttgggtc 929

gtgaatgatg ctcttttttt tcaacagcat ggaaaagcat atggagacga ccacacagtt 989

5

tgttacaccc accctgtgtt ccttgattca tttgaattct caggggtatc agtgacggat 1049

10

tcttctattc tttccctcta aggetcactt tcaggggtcc ttttctgaca aggtcacggg 1109

15

gctgtcctac agtctctgtc tgagcaatca caagccattc tctcaaaaac attaatactc 1169

20

aggcacatgc tgtatgtttt cactgtccgt cgtgtttttc acatttgtat gtgaaagggc 1229

25

ttgggggtggg atttgaagaa tgcacgatcg cctctgggtg atttcaataa aggatcttaa 1289

30

aatgcagatg aggactacga agaaatcact ctgaaaatga gttcacgcct caagaagcaa 1349

35

atccccctgga aacacagact ctttttcatt tttaatgtca ttagtttact cacagtctta 1409

40

tcaagaagaa gaggccaagg gttcaacca attttcagat cgcgtccctt aaacatcagt 1469

45

aattctgtta aagggatcaa acatccttat ttcttaacta actggtgcct tgctgtagag 1529

50

aaaggagcaa agcgcgccaga tccaaagtat atagttatca tagccaggaa ccgtactcg 1589

55

ttttccatta caaatggcaa attcttcccc gggtctcct catagtcct gagacggacc 1649

acggagggtga tgaacctccg gattctctgg cccaacacgg tggaagctct gcaagggcgc 1709

5 agagacagaa tgcggcagaa attgccccg agtcccaact ctcctttcct tgcgacctg 1769

10 ggaacaagac ttaaaggagc ctgtgactta gaaacttcta gtaatgggta cctggggagtc 1829

15 gtttgagtat ggggcagtga tttattctct gtgatggatg ccaacacggt taaacagaat 1889

20 ttttagtttt tatatgtgtg tgatgctgct cccccaaatt gttaactgtg taagagggtg 1949

25 gcaaaatagg gaaagtggca ttcacctata gttccagcat tcaggaagct gaggcaggag 2009

30 gattgtaaat ttgaggccag tctgagctgt aaggtagagac cctatttcaa acaacacagc 2069

35 gcaaggaaat gacgctttgc ccaacgaaat gtaggaaacc aacatagact cccagtttgt 2189

40 ccctctttat gtctgtctc cctaacaacg atctttgcta atgagaaaaa tattagaaaa 2249

45 aaatatccct gtgcaattat caccagtcg ccattataat gcaattaaaa ggcccacaag 2309

50 aaatcctgta tacacgaccg ttatttattg tatgtaagtt gctgaggaag aggagaaaaa 2369

55 aataaagatc atccattcct tcctgcaaaa aaaaaaaaaa aaanaaaaaa aaaaaaaaaa 2429

aaaaaaaaa a 2440

<210> 2

5 <211> 198

<212> PRT

10 <213> *Mus musculus*

15 <400> 2

Met Asp Ser Leu Leu Met Lys Gln Lys Lys Phe Leu Tyr His Phe Lys

1 5 10 15

20 Asn Val Arg Trp Ala Lys Gly Arg His Glu Thr Tyr Leu Cys Tyr Val

20 25 30

25 Val Lys Arg Arg Asp Ser Ala Thr Ser Cys Ser Leu Asp Phe Gly His

35 40 45

30 Leu Arg Asn Lys Ser Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr

50 55 60

35 Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp

65 70 75 80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Glu

40 85 90 95

Phe Leu Arg Trp Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg

45 100 105 110

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg

50 115 120 125

Leu His Arg Ala Gly Val Gln Ile Gly Ile Met Thr Phe Lys Asp Tyr

130 135 140

55

Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn Arg Glu Arg Thr Phe Lys

5 145 150 155 160

Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Thr Arg Gln Leu

10 165 170 175

Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala

15 180 185 190

Phe Arg Met Leu Gly Phe

195

20

25

<210> 3

<211> 30

30

<212> DNA

<213> Artificial Sequence

35

<220>

<223> Description of Artificial Sequence:Artificially

40

synthesized primer sequence, AID138

45

<400> 3

ggaattcgcc atggacagcc ttctgatgaa

30

50

<210> 4

55

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, AID161

<400> 4

gccgctcgag tcaaatccc aacatacgaa

30

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, AID118

<400> 5

ggctgagggtt agggttccat ctcag

25

<210> 6

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, AID119

<400> 6

gagggagtca agaaagtcac gctgg

25

<210> 7

<211> 2818

<212> DNA

<213> Homo sapiens

<220>

<221> 5' UTR

<222> (1).. (79)

<220>

<221> CDS

<222> (80).. (676)

<220>

<221> 3' UTR

<222> (677).. (2818)

5

<400> 7

10

agagaaccat cattaattga agtgagattt ttctggcctg agacttgcag ggaggcaaga 60

15

agacactctg gacaccact atg gac agc ctc ttg atg aac cgg agg aag ttt 112

Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe

1

5

10

20

ctt tac caa ttc aaa aat gtc cgc tgg gct aag ggt cgg cgt gag acc 160

Leu Tyr Gln Phe Lys Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr

25

15

20

25

30

tac ctg tgc tac gta gtg aag agg cgt gac agt gct aca tcc ttt tca 208

Tyr Leu Cys Tyr Val Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser

35

30

35

40

40

ctg gac ttt ggt tat ctt cgc aat aag aac ggc tgc cac gtg gaa ttg 256

Leu Asp Phe Gly Tyr Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu

45

50

55

45

ctc ttc ctc cgc tac atc tcg gac tgg gac cta gac cct ggc cgc tgc 304

Leu Phe Leu Arg Tyr Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys

50

60

65

70

75

55

tac cgc gtc acc tgg ttc acc tcc tgg agc ccc tgc tac gac tgt gcc 352

	Tyr Arg Val Thr Trp Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala	
5	80 85 90	
10	cga cat gtg gcc gac ttt ctg cga ggg aac ccc aac ctc agt ctg agg 400	
	Arg His Val Ala Asp Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg	
15	95 100 105	
20	atc ttc acc gcg cgc ctc tac ttc tgt gag gac cgc aag gct gag ccc 448	
	Ile Phe Thr Ala Arg Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro	
25	110 115 120	
30	gag ggg ctg cgg cgg ctg cac cgc gcc ggg gtg caa ata gcc atc atg 496	
	Glu Gly Leu Arg Arg Leu His Arg Ala Gly Val Gln Ile Ala Ile Met	
35	125 130 135	
40	acc ttc aaa gat tat ttt tac tgc tgg aat act ttt gta gaa aac cat 544	
	Thr Phe Lys Asp Tyr Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His	
45	140 145 150 155	
50	gaa aga act ttc aaa gcc tgg gaa ggg ctg cat gaa aat tca gtt cgt 592	
	Glu Arg Thr Phe Lys Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg	
55	160 165 170	
	ctc tcc aga cag ctt cgg cgc atc ctt ttg ccc ctg tat gag gtt gat 640	
	Leu Ser Arg Gln Leu Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp	
	175 180 185	

5 gac tta cga gac gca ttt cgt act ttg gga ctt tga tagcaacttc 686
 Asp Leu Arg Asp Ala Phe Arg Thr Leu Gly Leu
 190 195
 10
 caggaatgtc acacacgatg aaatatctct gctgaagaca gtggataaaa aacagtcctt 746
 15
 caagtcttct ctgtttttat tcttcaactc tcactttctt agagtttaca gaaaaaatat 806
 20
 ttatatacga ctcttttaaaa agatctatgt ctigaaaata gagaaggaac acaggtcttg 866
 25
 ccaggacgt gctgcaattg gtgcagtttt gaatgcaaca ttgtccccta ctgggaataa 926
 30
 cagaactgca ggacctggga gcacccctaaa gtgtcaacgt ttttctatga ctttaggta 986
 35
 ggatgagagc agaaggtaga tcctaaaaag catggtgaga ggatcaaag tttttatata 1046
 40
 aacatccttt attatttgat tcatttgagt taacagtggg gttagtata gatttttcta 1106
 45
 ttcttttccc ttgacgttta ctttcaagta acacaaactc ttccatcagg ccatgatcta 1166
 taggacctcc taatgagagt atctgggtga ttgtgacccc aaaccatctc tccaaagcat 1226
 50
 taatatccaa tcatgcgctg tatgttttaa tcagcagaag catgttttta tgttgtata 1286
 55
 aaagaagatt gttatgggtg gggatggagg tatagacat gcatggcac cttcaagcta 1346

5 ctttaataaa ggatcttaaa atgggcagga ggactgtgaa caagacaccc taataatggg 1406

10 ttgatgtctg aagtagcaaa tcttctggaa acgcaaactc ttttaaggaa gtccctaatt 1466

15 tagaaacacc cacaaacttc acatatcata attagcaaac aattggaagg aagttgcttg 1526

20 aatgttgggg agaggaaaat ctattggctc tcgtgggtct cttcatctca gaaatgccaa 1586

25 tcaggtaag gtttgctaca tttgtatgt gtgtgatgct tctcccaaag gtatattaac 1646

30 tatataagag agttgtgaca aaacagaatg ataaagctgc gaaccgtggc acacgctcat 1706

35 agttctagct gcttgggagg ttgaggagg aggatggctt gaacacaggt gttcaaggcc 1766

40 agcctgggca acataacaag atcctgtctc tcaaaaaaaaa aaaaaaaaaa aagaaagaga 1826

45 gagggccggg cgtggtggct cacgcctgta atcccagcac tttgggaggc cgagccgggc 1886

50 ggatcacctg tggtcaggag tttgagacca gcctggccaa catggcaaaa ccccgctctg 1946

55 actcaaaatg caaaaattag ccaggcgtgg tagcaggcac ctgtaatccc agctacttgg 2006

 gaggctgagg caggagaatc gcttgaacc aggaggtgga ggttgcaagta agctgagatc 2066

 gtgccgtgc actccagcct gggcgacaag agcaagactc tgtctcagaa aaaaaaaaaa 2126

5 aaaagagaga gagagagaaa gagaacaata tttgggagag aaggatgggg aagcattgca 2186
 10 aggaaattgt gctttatcca acaaaatgta aggagccaat aagggatccc tatttgtctc 2246
 15 ttttggtgtc tatttgtccc taacaactgt ctttgacagt gagaaaaata ttcagaataa 2306
 20 ccatatccct gtgccgttat tacctagcaa cccttgcaat gaagatgagc agatccacag 2366
 25 gaaaacttga atgcacaact gtcttatttt aatcttattg tacataagtt tgtaaaagag 2426
 30 ttaaaaattg ttacttcatg tattcattta tattttatat tattttgcgt ctaatgattt 2486
 35 tttattaaca tgatttcctt ttctgatata ttgaaatgga gtctcaaagc ttcataaatt 2546
 40 tataacttta gaaatgattc taataacaac gtatgtaatt gtaacattgc agtaatggtg 2606
 45 tcactttcaa tcagttaaatt aaatgataaa taattttgga agctgtgaag ataaaatacc 2726
 50 aaataaaata atataaaagt gatttatatg aagttaaaat aaaaaatcag tatgatggaa 2786
 55 taaacttgaa aaaaaaaaaa aaaaaaaaaa aa 2818

<210> 8

<211> 198

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys

1 5 10 15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val

20 25 30

Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr

35 40 45

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr

50 55 60

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp

65 70 75 80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp

85 90 95

Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg

100 105 110

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg

115 120 125

Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr

130 135 140

Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys

145 150 155 160

Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu

5

165

170

175

Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala

10

180

185

190

Phe Arg Thr Leu Gly Leu

15

195

20

<210> 9

25

<211> 5514

<212> DNA

30

<213> Homo sapiens

35

<220>

<221> intron

<222> (1)..(1031)

40

<220>

45

<221> exon

<222> (1032)..(1118)

50

<220>

<221> intron

55

<222> (1119)..(5514)

<400> 9

5 acagacgaat acatgggtcca agctagggct attgatttga aaatcatcaa ggtatagatg 60
 gtatcaaagg cttgaggcag gaagagagca gagaccctag ctgcattgct tagcattgca 120
 10 tccctagcac ctggcatagt ttccattaac agtaggcatg aagtatctac tcagtgaata 180
 aatagaatgc atatgggcta cagtaggaga gagaaataaa atctttaata gaccaagttc 240
 tatgagagca caaaattaaa gtcttttatt tgaagatctt agcctgtttt ccaaattcag 300
 15 tgcagccagt tagacactga ttctgtctgg tgaacaagc atttttgtat tttgggggac 360
 tgctgtctgt tctgactcca aattaaggat ttttttttt tctaaaaaag atggctcatg 420
 20 caaaaatcac tctttgggtg aaatatctag tcttcaagca attcttgtaa tgcaatcaga 480
 aagaaaaaaa tccatgggtt gggaggcaaa atttttgtgt tctaaattct atataactga 540
 gttcatttgc ttaactgcaa agcaggagct gctagtcct gtctgtactg aggttcagag 600
 25 agactgtggg aatatggggg aattagaggc tatctgaggc tcttcaacac aataacccaa 660
 gaagctattt aaatgctctt taaggatatt acataaatat tactattctc attgtgcttt 720
 30 tatittgtgt tatcatgatt ataattgaag tgtctactgt tactgcctcc tgatctttgc 780
 tagctatgga gcatggactg ggctttttaga gcagcagccc caaaggaacc taaacattaa 840
 agcagagctg ccctcaatgg tttaacctgt gtgactctgc ctatgacagc cccaccacc 900
 35 catcttcact ggatccaaat caggagcaag gccgttgggg tacctggtgg gggtgatgct 960
 gtcaggggag gagcccaaaa gggcaagctc aaatttgaat gtgaagggcc aatgcactgt 1020
 40 cagactgaga cagagaacca tcattaattg aagtgaattt tttctggcct gagacttgca 1080
 gggaggcaag aagacactct ggacaccact atggacaggt aaagaggcag tcttctcgtg 1140
 45 ggtgattgca ctggccttcc tctcagagca aatctgagta atgagactgg tagctatccc 1200
 tttctctcat gtaactgtct gactgataag atcagcttga tcaatatgca tatatatttt 1260
 50 ttgatctgtc tccttttctt ctattcagat cttatacgct gtcagcccaa tcttttctgt 1320
 ttcagacttc tcttgatttc cctctttttc atgtggcaaa agaagtagtg cgtacaatgt 1380
 actgattcgt cctgagattt gtaccatggt tgaaactaat ttatggtaat aatattaaca 1440
 55 tagcaaatct ttagagactc aaatcatgaa aaggtaatag cagtactgta ctaaaaacgg 1500

tagtgctaatt tttcgtaata attttgtaaa tattcaacag taaaacaact tgaagacaca 1560
 5 ctttcctagg gaggcgttac tgaataatt tagctatagt aagaaaattt gtaatttttag 1620
 aaatgccaaag cattctaaat taattgcttg aaagtcacta tgattgtgtc cattataagg 1680
 agacaaattc attcaagcaa gttatttaatt gttaaaggcc caattggttag gcagttaatg 1740
 10 gcactttttac tattaactaa tctttccatt tgttcagacg tagcttaact tacctcttag 1800
 gtgtgaattt ggtaaggtc ctcataatgt ctttatgtgc agtttttgat aggttattgt 1860
 15 catagaactt attctattcc tacatttatg attactatgg atgtatgaga ataacaccta 1920
 atccttatac ttacctcaa ttaactcct ttataaagaa cttacattac agaataaaga 1980
 20 ttttttaaaa atatattttt ttgtagagac agggctcttag cccagccgag gctggtctct 2040
 aagtcctggc ccaagcgatc ctctgcctg ggccctcctaa agtgctggaa ttatagacat 2100
 gagccatcac atccaatata cagaataaag atttttaatg gaggatttaa tgttcttcag 2160
 25 aaaattttct tgaggtcaga caatgtcaaa tgtctcctca gtttacctg agattttgaa 2220
 aacaagtctg agctataggt ccttggaag ggtccattgg aaatacttgt tcaaagtaaa 2280
 30 atggaaagca aaggtaaaat cagcagttga aattcagaga aagacagaaa aggagaaaag 2340
 atgaaattca acaggacaga agggaaatat attatcatta aggaggacag tatctgtaga 2400
 gctcattagt gatggcaaaa tgacttggtc aggattattt ttaacccgct tgtttctggt 2460
 35 ttgcacggct ggggatgcag ctagggttct gcctcagga gcacagctgt ccagagcagc 2520
 tgtcagcctg caagcctgaa acactccctc ggtaaagtcc ttcctactca ggacagaaat 2580
 40 gacgagaaca gggagctgga aacaggcccc taaccagaga agggaagtaa tggatcaaca 2640
 aagttaacta gcaggtcagg atcacgcaat tcatittact ctgactggta acatgtgaca 2700
 45 gaaacagtgt aggcattatg tattttcatg tagagtagga cccaaaaatc cacccaaagt 2760
 cctttatcta tgccacatcc ttcttatcta tacttccagg acactttttc ttccttatga 2820
 taaggctctc tctctctcca cacacacaca cacacacaca cacacacaca cacacacaca 2880
 50 cacaacaca caccgcgcca accaagggtc atgtaaaaag atgtagattc ctctgccttt 2940
 ctcatctaca cagcccagga gggtaagtta atataagagg gatttattgg taagagatga 3000
 55 tgettaatct gittaacact gggcctcaaa gagagaattt cttttcttct gtacttatta 3060

agcacctatt atgtgttgag cttatatata caaagggtta ttatatgcta atatatgaat 3120
 5 agtaatgktg gttggacta tggtaattac cataaaaatt awtatccttt taaaataaag 3180
 ctaattatta ttggatcttt tttagtatte attttatgtt ttttatgttt ttgatttttt 3240
 10 aaaagacaat ctcaccctgt taccaggtt ggagtgcagt ggtgcaatca tagctttctg 3300
 cagtcttgaa ctcctgggct caagcaatcc tcctgccttg gcctcccaa gtgttgggat 3360
 acagtcatga gccactgcat ctggcctagg atccatttag attaaaatat gcattttaaa 3420
 15 ttttaaaata atattgctaa tttttacctt atgtaatgtg tatactggta ataaatctag 3480
 tttgctgcct aaagttaaa gtgctttcca ataagcttca tgtacgtgag gggagacatt 3540
 20 taaagtgaag cagacagcca ggtgtgtgtg ctcacgcctg taatcccagc actctgggag 3600
 gctgaggttg gtggatcgct tgagccctgg agttcaagac cagcctgagc aacatggcaa 3660
 aaccctgttt ctataacaaa aattagccgg gcatgtgtgg atgtgcctgt ggtcccagct 3720
 25 actagggggc tgaggcagga gaattcttgg agcccaggag gtcaaggctg cactgagcag 3780
 tgcttgccc actgcactcc agcctgggtg acaggaccag acctgcctc aaaaaataa 3840
 30 gaagaaaaat taaaaataa tggaacaac tacaaagagc tgttgtccta gatgagctac 3900
 ttagttaggc tgatatcttg gtatttaact tttaaagtca ggtgtgtc cctgcactac 3960
 attattaaaa tatcaattct caatgtatat ccacacaaag actggtacgt gaattgtcat 4020
 35 agtaccttta ttcacaaaac ccaaagtag agactatcca aatatccatc aacaagtga 4080
 caaataaaca aaatgtgcta tatccatgca atggaatacc accctgcagt acaaaggaag 4140
 40 aagctacttg gggatgaatc ccaaagtcac gacgctaaat gaaagagtca gacatgaag 4200
 aggagataat gtatgccata cgaaattcta gaaatgaaa gtaacttata gttacagaaa 4260
 45 gcaaatacag gcaggcatag aggctcacac ctgtaatccc agcactttga gaggccacgt 4320
 gggaagattg ctagaactca ggagtccaag accagcctgg gcaacacagt gaaactccat 4380
 tctccacaaa aatgggaaaa aaagaaagca aatcagtgtg tgcctgttg ggaggggaag 4440
 50 gactgcaaag aggggaagag cctctgtgtg gtgaggtgtg tgattcaggt tctgtatcct 4500
 gactgtgtga gcagtttggg gtgtttacat caaaaaatat tcgtagaatt atgcatctta 4560
 55 aatgggtgga gtttactgta tgtaaattat acctcaatgt aagaaaaaat aatgtgtaag 4620

aaaagtttca attctcttgc cagcaaacgt tattcaaatt cctgagccct ttacttcgca 4680
 5 aattctctgc acttctgccc cgtaccatta ggtgacagca ctagctccac aaattggata 4740
 aatgcatttc tggaaaagac tagggacaaa atccaggcat cacttgtgct ttcatatcaa 4800
 10 ccacgctgta cagcttgtgt tgctgtctgc agctgcaatg gggactcttg atttctttaa 4860
 ggaaacttgg gttaccagag tatttcaca aatgctatc aaattagtgc ttatgatatg 4920
 caagacactg tgctaggagc cagaaaacaa agaggaggag aaatcagtca ttatgtggga 4980
 15 acaacatagc aagatattta gatcatittg actagttaaa aaagcagcag agtacaaaat 5040
 cacacatgca atcagtataa tccaaatcat gtaaatatgt gcctgtagaa agactagagg 5100
 20 aataaacaca agaattctaa cagtcattgt cattagacac taagtctaatt tattattatt 5160
 agacactatg atatttgaga tttaaaaaat ctttaatat tttaaattta gagctcttct 5220
 atttttccat agtattcaag tttgacaatg atcaagtatt actctttctt tttttttttt 5280
 25 tttttttttt tttgagatgg agttttggtc ttgttgccca tgctggagtg gaatggcatg 5340
 aycatagctc actgcaacct ccacctcctg ggttcaagca aagctgtcgc ctcagcctcc 5400
 30 cgggtagatg ggattacagg cgcccaccac cacactcggc taatgtttgt atttttagta 5460
 gagatggggt ttcacatgt tggccaggct ggtctcaaac tcctgacctc agag 5514

40 <210> 10

<211> 6564

<212> DNA

45 <213> Homo sapiens

50 <400> 10

gggggcctgt aatcccagct actcaggagg ctgaggcagg aggatccgcg gagcctggca 60
 gatctgcctg agcctgggag gttgaggcta cagtaagcca agatcatgcc agtatacttc 120
 55 agcctgggcg acaaaagttag accgtaacaa aaaaaaaaaa atttaaaaaa agaaatttag 180

atcaagatcc aactgtaaaa agtggcctaa acaccacatt aaagagttag gagtttattc 240
 5 tgcaggcaga agagaacccat cagggggctct tcagcatggg aatggcatgg tgcacctggg 300
 ttttgtgaga tcatgggtgg gacagtgtgg ggaatgttat tttggaggga ctggaggcag 360
 10 acagaccggt taaaaggcca gcacaacaga taaggaggaa gaagatgagg gcttgaccg 420
 aagcagagaa gagcaaacag ggaaggatca aattcaagaa atattggggg gtttgaatca 480
 acacatttag atgattaatt aaatatgagg actgaggaat aagaaatgag tcaaggatgg 540
 15 ttccagctg ctaggctgct tacctgaggt ggcaaagtcg ggaggagtgg cagtttagga 600
 cagggggcag ttgaggaata ttgttttgat cattttgagt ttgaggtaca agttggacac 660
 20 ttaggtaaag actggagggg aaatctgaat atacaattat gggactgagg aacaagtta 720
 ttttattttt tgtttcggtt tcttgttgaa gaacaaattt aattgtaatc ccaagtcac 780
 25 agcatctaga agacagtggc aggaggtgac tgtcttggg gtaagggttt ggggtccttg 840
 atgagtatct ctcaattggc cttaaataata agcaggaaaa ggagtttatg atggattcca 900
 ggctcagcag ggctcaggag ggctcaggca gccagcagag gaagtcagag catcttcttt 960
 30 ggtttagccc aagtaatgac ttccttaaaa agctgaagga aaatccagag tgaccagatt 1020
 ataaactgta ctcttgcat tctctccct cctctcacc acagcctctt gatgaaccgg 1080
 35 aggaagttag tttaccaatt caaaaatgac cgctgggcta agggtcggcg tgagacctac 1140
 ctgtgctacg tagtgaagag gcgtgacagt gctacatcct tttactgga ctttgggtat 1200
 cttcgcaata aggtatcaat taaagtcagc ttgcaagca gttaaatggt caactgtgag 1260
 40 tgcttttaga gccacctgct gatggtatta ctccatcct tttttggcat ttgtgtctct 1320
 atcacattcc tcaaatcctt ttttttattt ctttttccat gtccatgcac ccatattaga 1380
 45 catggcccaa aatatgtgat ttaattcctc ccagtaatg ctgggcaccc taataccact 1440
 ccttccttca gtgccaagaa caactgctcc caaactgttt accagctttc ctcagcatct 1500
 50 gaattgcctt tgagattaat taagctaaaa gcatttttat atgggagaat attatcagct 1560
 tgtccaagca aaaattttta atgtgaaaa caaattgtgt ctttaagcatt ttgaaaatt 1620
 aaggaagaag aatttgggaa aaaattaacg gtggttcaat tctgttttcc aaatgatttc 1680
 55 ttttcctcc tactcacatg ggtcgtaggc cagtgaatac attcaacatg gtgatcccca 1740

gaaaaactcag agaagcctcg gctgatgatt aattaaattg atctttcggc tacccgagag 1800
 5 aattacattt ccaagagact tcttcaccaa aatccagatg ggtttacata aacttctgcc 1860
 catgggtatc tcctctctcc taacacgctg tgacgtctgg gcttggtgga atctcaggga 1920
 10 agcatccgtg ggggtgaagg tcacgtctcg gctcgttggt tgatggttat attaccatgc 1980
 aattttcttt gcctacattt gtattgaata catcccaatc tccttcctat tcggtgacat 2040
 gacacattct atttcagaag gctttgattt tatcaagcac ttcatattac ttctcatggc 2100
 15 agtgcctatt acttctctta caatacccat ctgtctgctt taccaaaatc tatttcccct 2160
 tttcagatcc tcöcaaatgg tcctcataaa ctgtcctgcc tccacctagt ggtccaggta 2220
 20 tatttccaca atgttacatc aacaggcact tctagccatt ttcttctca aaaggtgcaa 2280
 aaagcaactt cataaacaca aattaaatct tcggtgaggt agtgtgatgc tgcttcctcc 2340
 caactcagcg cacttcgtct tcctcattcc aaaaaaacc atagccttcc ttactctgc 2400
 25 aggactagtg ctgccaaggg ttcagctcta cctactggtg tgctcttttg agcaagttgc 2460
 ttagcctctc tgtaacacaa ggacaatagc tgcaagcatc cccaaagatc attgcaggag 2520
 30 acaatgacta aggtaccag agccgcaata aaagtcagtg aatttttagcg tggctcctc 2580
 tgtctctcca gaacggctgc cacgtggaat tgctcttctt ccgtacatc tcggactggg 2640
 35 acctagaccc tggcgcgtgc tacgcgtca cctggttac ctctggagc ccctgctacg 2700
 actgtgcccg acatgtggcc gactttctgc gagggaaacc caacctcagt ctgaggatct 2760
 tcaccgcgcg cctctacttc tgtgaggacc gcaaggctga gcccgagggg ctgcggcggc 2820
 40 tgcaccgcgc cggggtgcaa atagccatca tgacctcaa aggtgcgaaa gggccttccg 2880
 cgcaggcgca gtgcagcagc ccgcattcgg gattgcgatg cggaatgaat gagttagtgg 2940
 45 ggaagctcga ggggaagaag tgggcgggga ttctggttca cctctggagc cgaaattaaa 3000
 gattagaagc agagaaaaga gtgaatggct cagagacaag gccccgagga aatgagaaaa 3060
 50 tggggccagg gttgcttctt tcccctcgat ttggaacctg aactgtcttc taccata 3120
 tcccgcctt ttttcttt ttttttttt tgaagattat ttttactgct ggaatacttt 3180
 tgtagaaaac cacgaaagaa ctttcaaagc ctgggaaggg ctgcatgaaa attcagttcg 3240
 55 tctctccaga cagcttcggc gcactctttt ggtaaggggc ttctctgctt tttaaatttt 3300

ctttctttct ctacagtctt ttttggagtt tcgtatattt cttatatattt cttattgttc 3360
 5 aatcacctctc agttttcatc tgatgaaaac tttatttctc ctccacatca gctttttctt 3420
 ctgctgtttc accattcaga gccctctgct aaggttcctt ttcctccctt tttctttctt 3480
 10 ttgttgtttc acatctttta atttctgtct ctccccaggg ttgcgtttcc ttcctgggtca 3540
 gaattctttt ctcccttttt tttttttttt tttttttttt taaacaaaca aacaaaaaac 3600
 ccaaaaaaac tctttcccaa tttactttct tccaacatgt tacaagcca tccactcagt 3660
 15 ttagaagact ctccggcccc accgaccccc aacctcgttt tgaagccatt cactcaattt 3720
 gcttctctct tctctacag cccctgtatg aggttgatga cttacgagac gcatttcgta 3780
 20 ctttgggact ttgatagcaa ctccaggaa tgcacacac gatgaaatat ctctgctgaa 3840
 gacagtggat aaaaaacagt cttcaagtc ttctctgttt ttattcttca actctcactt 3900
 tcttagagtt tacagaaaaa atatttatat acgactcttt aaaaagatct atgtcttgaa 3960
 25 aatagagaag gaacacaggt ctggccaggg acgtgctgca attggtgcag ttttgaatgc 4020
 aacattgtcc cctactggga ataacagaac tgcaggacct gggagcatcc taaagtgtca 4080
 30 acgtttttct atgactttta ggtaggatga gagcagaagg tagatcctaa aaagcatggt 4140
 gagaggatca aatgttttta tatcaacatc ctttattatt tgattcattt gagttaacag 4200
 35 tgggtgtagt gatagatttt tctattcttt tcccttgacg tttactttca agtaacacaa 4260
 actcttccat caggccatga tetataggac ctctaatga gagtatctgg gtgattgtga 4320
 ccccaaacca tctctccaaa gcattaatat ccaatcatgc gctgtatgtt ttaatcagca 4380
 40 gaagcatggt tttatgtttg taaaaagaa gattgttatg ggtggggatg gaggtataga 4440
 ccatgcatgg tcaccttcaa gctactttta taaaggatct taaaatgggc aggaggactg 4500
 45 tgaacaagac accctaataa tgggttgatg tctgaagtag caaatcttct ggaaacgcaa 4560
 actcttttaa ggaagtcctt aatttagaaa caccacaaa cttcacatat cataattagc 4620
 50 aaacaattgg aaggaagttg ctigaatgtt ggggagagga aaatctattg gctctcgtgg 4680
 gtctcttcat ctcagaaatg ccaatcaggt caaggtttgc tacattttgt atgtgtgtga 4740
 tgcttctccc aaaggtatat taactatata agagagttgt gacaaaacag aatgataaag 4800
 55 ctgcgaaccg tggcacacgc tcatagttct agctgcttgg gaggttgagg agggaggatg 4860

gcttgaacac aggtgttcaa ggccagcctg ggcaacataa caagatcctg tctctcaaaa 4920
 5 aaaaaaaaaa aaaaaagaaa gagagagggc cgggcgtggt ggctcacgcc tgtaatccca 4980
 gcactttggg aggccgagcc gggcggatca cctgtggtca ggagtttgag accagcctgg 5040
 10 ccaacatggc aaaaccccgt ctgtactcaa aatgcaaaaa ttagccaggc gtggtagcag 5100
 gcacctgtaa tcccagctac ttgggaggct gaggcaggag aatcgcttga acccaggagg 5160
 tggagggtgc agtaagctga gatcgtgccg ttgcactcca gcctgggcga caagagcaag 5220
 15 actctgtctc agaaaaaaaa aaaaaaaga gagagagaga gaaagagaac aatatttggg 5280
 agagaaggat ggggaagcat tgcaaggaaa ttgtgcttta tccaacaaaa tgtaaggagc 5340
 20 caataaggga tccctatttg tctcttttgg tgtctatttg tccctaacaa ctgtctttga 5400
 cagtgagaaa aatattcaga ataaccatat ccctgtgccg ttattaccta gcaacccttg 5460
 caatgaagat gagcagatcc acaggaaaac ttgaatgcac aactgtctta ttttaattct 5520
 25 attgtacata agtttgtaaa agagttaaaa attgttactt catgtattca tttatatatt 5580
 atattatttt gcgtctaattg attttttatt aacatgattt ccttttctga tatattgaaa 5640
 30 tggagtctca aagcttcata aatttataac tttagaaatg attctaataa caacgtatgt 5700
 aattgtaaca ttgcagtaat ggtgctacga agccatttct cttgatTTTT agtaaacttt 5760
 35 tatgacagca aatttgcttc tggtcactt tcaatcagtt aaataaatga taaataattt 5820
 tggaagctgt gaagataaaa taccaataaa aataatataa aagtgattta tatgaagta 5880
 aaataaaaaa tcagtatgat ggaataaact tgagagtcca gaagttatcc catacatctg 5940
 40 taatcaacta atttctcaca aggggtgtaag gaccattcaa tggagaaaaa atgatcttct 6000
 caacaaatgg tgctgagcta attggatatt acatgcaaag gaatgaattt gagtctctac 6060
 45 tacacaccat atataaaaaat taattaaaaa ttcatcaaat acctaaatat tagagactaa 6120
 tttataaacc gtagagagaa acataggtaa aatgtttat ggcttttagat taggcaacag 6180
 cttcttaatt atgacatcaa aagcacaagc aaccaaagac aaaaataaat cagttggact 6240
 50 tcatcgaaat taaaaatctt tgtgcatcaa aggacactta gtaagaaagt gaaaagacaa 6300
 cccacagaag tgggagaaaa cacttgcaaa tcatatatct gataagggtt gtgatattat 6360
 55 gatatatata taggtttttg tccatagttc ctggttata aacccctca cccttgttac 6420

agtcatttgt tataagggtg gatggtttag gcctcagaag caaaactctc tctctcacct 6480
 5 tctccagccc tctgtctctt ggcacctcat tcttccctga ggccacatag aaactagaat 6540
 ctctctttcca caaggcggtc aaag 6564

10
 15 <210> 11

<211> 87

<212> DNA

20 <213> Homo sapiens

25 <400> 11

agagaaccat cattaattga agtgagattt ttctggcctg agacttgcag ggaggcaaga 60
 30 agacactctg gacaccacta tggacag 87

35 <210> 12

<211> 148

40 <212> DNA

<213> Homo sapiens

45 <400> 12

cctcttgatg aaccggagga agtttcttta ccaattcaaa aatgtccgct gggctaaggg 60
 50 tcggcgtgag acctacctgt gctacgtagt gaagaggcgt gacagtgcta catccttttc 120
 actggacttt ggttatcttc gcaataag 148

<210> 13

<211> 271

<212> DNA

<213> Homo sapiens

<400> 13

```

aacggctgcc acgtggaatt gctcttcctc cgctacatct cggactggga cctagaccct 60
ggccgctgct accgcgtcac ctggttcacc tcctggagcc cctgctacga ctgtgcccga 120
catgtggccg actttctgcg aggggaacccc aacctcagtc tgaggatctt caccgcgcgc 180
ctctacttct gtgaggaccg caaggctgag cccgaggggc tgcggcggct gcaccgcgcc 240
ggggtgcaaa tagccatcat gaccttcaaa g                               271

```

<210> 14

<211> 116

<212> DNA

<213> Homo sapiens

<400> 14

```

attatittta ctgctggaat actttttag aaaaccacga aagaactttc aaagcctggg 60
aagggtgca tgaaaattca gttcgtctct ccagacagct tcggcgcatc cttttg    116

```

<210> 15

<211> 2172

<212> DNA

<213> Homo sapiens

5

<400> 15

10

cccctgtatg aggttgatga cttacgagac gcatttcgta ctttgggact ttgatagcaa 60

cttccaggaa tgtcacacac gatgaaatat ctctgctgaa gacagtggat aaaaaacagt 120

ccttcaagtc ttctctgttt ttattcttca actctcaatt tcttagagtt tacagaaaaa 180

15

atatttatat acgactcttt aaaaagatct atgtcttgaa aatagagaag gaacacaggt 240

ctggccaggg acgtgctgca attgggtgcag ttttgaatgc aacattgtcc cctactggga 300

20

ataacagaac tgcaggacct gggagcatcc taaagtgtca acgtttttct atgactttta 360

ggtaggatga gacagaagg tagatcctaa aaagcatggt gagaggatca aatgttttta 420

25

tatcaacatc ctttattatt tgattcattt gagttaacag tgggtgtagt gatagatttt 480

tctattcttt tcccttgacg tttactttca agtaacacaa actcttccat caggccatga 540

tctataggac ctctaatga gagtatctgg gtgattgtga ccccaaacca tctctccaaa 600

30

gcattaatat ccaatcatgc gctgtatgtt ttaatcagca gaagcatgtt tttatgtttg 660

tacaaaagaa gattgttatg ggtggggatg gaggtataga ccatgcatgg tcaccttcaa 720

35

gctactttta taaaggatct taaaatgggc aggaggactg tgaacaagac accctaataa 780

tgggttgatg tctgaagtag caaatcttct ggaaacgcaa actcttttaa ggaagtcct 840

aatttagaaa caccacaaa cttcacatat cataattagc aaacaattgg aaggaagttg 900

40

cttgaatgtt ggggagagga aaatctattg gctctcgtgg gtctcttcat ctcagaaatg 960

ccaatcaggt caaggtttgc tacattttgt atgtgtgtga tgcttctccc aaaggtatat 1020

45

taactatata agagagttgt gacaaaacag aatgataaag ctgcgaaccg tggcacacgc 1080

tcatagtctt agctgcttgg gaggttgagg agggaggatg gcttgaacac aggtgttcaa 1140

ggccagcctg ggcaacataa caagatcctg tctctcaaaa aaaaaaaaaa aaaaaagaaa 1200

50

gagagagggc cgggcgtggt ggctcacgcc tgtaatccca gcactttggg aggccgagcc 1260

gggcggatca cctgtggtca ggagtttgag accagcctgg ccaacatggc aaaaccccg 1320

55

ctgtactcaa aatgcaaaaa ttagccaggc gtggtagcag gcacctgtaa tccagctac 1380

ttgggaggct gaggcaggag aatcgcttga acccaggagg tggaggttgc agtaagctga 1440
 gatcgtgccg ttgcactcca gcctgggcga caagagcaag actctgtctc agaaaaaaaa 1500
 aaaaaaaaaa gagagagaga gaaagagaac aatatttggg agagaaggat ggggaagcat 1560
 tgcaaggaaa ttgtgcttta tccaacaaaa tgtaaggagc caataaggga tccctatttg 1620
 tctcttttgg tgtctatttg tccctaacaa ctgtctttga cagtgaagaa aatattcaga 1680
 ataaccatat ccctgtgccg ttattaccta gcaacccttg caatgaagat gagcagatcc 1740
 acaggaaaac ttgaatgcac aactgtctta ttttaatctt attgtacata agtttgtaaa 1800
 agagttaaaa attgttactt catgtattca tttatatatt atattatttt gcgtctaatt 1860
 attttttatt aacatgattt ccttttctga tatattgaaa tggagtctca aagcttcata 1920
 aatttataac tttagaaatg attctaataa caacgtatgt aattgtaaca ttgcagtaat 1980
 ggtgctacga agccatttct ctgtattttt agtaaacctt tatgacagca aatttgcttc 2040
 tggctcactt tcaatcagtt aaataaatga taaataattt tggaagctgt gaagataaaa 2100
 taccaaataa aataatataa aagtgattta tatgaagtta aaataaaaaa tcagtatgat 2160
 ggaataaaact tg 2172

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
 synthesized primer sequence, 170

<400> 16

gagaccgata tggacagcct tctga

25

5

<210> 17

10

<211> 27

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
syntjesized primer sequence, 181

25

<400> 17

30

tcacgtgtga cattccagga ggttgct

27

35

<210> 18

<211> 30

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, 22

50

55

<400> 18

gtagtgaaga ggcgtgacag tgctacatcc

30

5

<210> 19

10

<211> 27

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, 25

25

<400> 19

30

gttccctcgc agaaagtcgg ccacatg

27

35

<210> 20

<211> 24

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p3

50

55

<400> 20

gagtttgagg tacaagttgg acac

24

5

10

<210> 21

<211> 23

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p9

25

<400> 21

30

tatctcctct ctccatacac gct

23

35

<210> 22

<211> 23

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p10

50

55

<400> 22

acaagctgat aatattctcc cat

23

5

<210> 23

10

<211> 22

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, pl2

25

<400> 23

30

tcttcggtga ggtagtgtga tg

22

35

<210> 24

<211> 30

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, pl4

50

55

<400> 24

agcctcttga tgaaccggag gaagtttctt

30

5

<210> 25

10

<211> 28

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, pl6

25

<400> 25

30

ttattgcgaa gataaccaaa gtccagtg

28

35

<210> 26

<211> 21

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, pl7

50

55

<400> 26

tagaccctgg ccgctgctac c

21

5

<210> 27

10

<211> 22

<212> DNA

15

<213> Artificial Sequence

<220>

20

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p19

25

<400> 27

30

cgcacgcgcaa tcccgaatgc gg

22

35

<210> 28

<211> 28

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p26

50

55

<400> 28

caaaaggatg cgccgaagct gtctggag

28

5

<210> 29

10

<211> 23

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p29

25

<400> 29

30

gttggaagaa agtaaattgg gaa

23

35

<210> 30

<211> 21

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p36

50

55

<400> 30

gatactctca ttaggaggtc c

21

5

<210> 31

10

<211> 26

<212> DNA

15

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p48

25

<400> 31

30

cattaattga agtgagattt ttctgg

26

35

<210> 32

<211> 22

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p59

50

55

<400> 32

agcatttgtg gaaatactct gg

22

5

<210> 33

10

<211> 24

<212> DNA

15

<213> Artificial Sequence

<220>

20

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p85

25

<400> 33

30

aactttattt ctcctccaca tcag

24

35

<210> 34

<211> 21

40

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence:Artificially
synthesized primer sequence, p86

50

<400> 34

55

gtgaatggct cagagacaag g

21

5

<210> 35

10

<211> 11204

<212> DNA

15

<213> Homo sapiens

<400> 35

20

aggttcagag agactgtggg aatatggggg aattagaggc tatctgaggc tcttcaacac 60

aataacccaa gaagctatctt aaatgctctt taaggatctt acataaatat tactattctc 120

25

attgtgcttt tattttgtgt tatcatgatt ataattgaag tgtctactgt tactgcctcc 180

tgatctttgc tagctatgga gcatggactg ggcttttaga gcagcagccc caaaggaacc 240

30

taaacattaa agcagagctg ccctcaatgg ttttaacctgt gtgactctgc ctatgacagc 300

cccacccacc catcttcact ggatccaaat caggagcaag gccgttgggg tacctggtgg 360

35

gggtgatgct gtcaggggag gagcccaaaa gggcaagctc aaatttgaat gtgaagggcc 420

aatgcactgt cagactgaga cagagaacca tcattaattg aagtgaagatt tttctggcct 480

gagacttgca gggaggcaag aagacactct ggacaccact atggacaggt aaagaggcag 540

40

tcttctcgtg ggtgattgca ctggccttcc tctcagagca aatctgagta atgagactgg 600

tagctatccc tttctctcat gtaactgtct gactgataag atcagcttga tcaatatgca 660

45

tatatatctt ttgatctgtc tccttttctt ctattcagat cttatacgt gtcagcccaa 720

ttctttctgt ttcagacttc tcttgatttc cctctttttc atgtggcaaa agaagtagtg 780

cgtacaatgt actgattcgt cctgagattt gtaccatggt tgaaactaat ttatggtaat 840

50

aatattaaca tagcaaatct ttagagactc aaatcatgaa aaggtaatag cagtactgta 900

ctaaaaacgg tagtgctaatt tttcgtaata attttgtaaa tattcaacag taaaacaact 960

55

tgaagacaca ctttcctagg gaggcgttac tgaataat tagctatagt aagaaaattt 1020

gtaatttttag aaatgccaag cattctaaat taattgcttg aaagtcacta tgattgtgtc 1080
 5 cattataagg agacaaattc attcaagcaa gttatttaat gttaaaggcc caattgttag 1140
 gcagttaatg gcacttttac tattaactaa tctttccatt tgttcagacg tagcttaact 1200
 10 tacctcttag gtgtgaattt ggtaaggctc ctcataatgt ctttatgtgc agtttttgat 1260
 aggttattgt catagaactt attctattcc tacatttatg attactatgg atgtatgaga 1320
 ataacaccta atccttatac tttacctcaa tttactcct ttataaagaa cttacattac 1380
 15 agaataaaga ttttttaaaa atatattttt ttgtagagac agggctcttag cccagccgag 1440
 gctggtctct aagtccctggc ccaagcgatc ctccctgctg ggccctcctaa agtgctggaa 1500
 20 ttatagacat gagccatcac atccaatata cagaataaag atttttaatg gaggatttaa 1560
 tgttcttcag aaaattttct tgaggtcaga caatgtcaaa tgtctcctca gtttacctg 1620
 agattttgaa aacaagctcg agctataggt ccttggaag ggtccattgg aaatacttgt 1680
 25 tcaaagtaaa atggaaagca aaggtaaaat cagcagttga aattcagaga aagacagaaa 1740
 aggagaaaag atgaaattca acaggacaga agggaaatat attatcatta aggaggacag 1800
 30 tatctgtaga gctcattagt gatggcaaaa tgacttggtc aggattattt ttaacccgct 1860
 tgtttctggt ttgcacggct ggggatgcag ctagggttct gcctcagga gcacagctgt 1920
 ccagagcagc tgtcagcctg caagcctgaa aactccctc ggtaaagtcc ttcctactca 1980
 35 ggacagaaat gacgagaaca gggagctgga aacaggcccc taaccagaga agggaagtaa 2040
 tggatcaaca aagttaacta gcaggtcagg atcacgcaat tcatttcact ctgactggta 2100
 40 acatgtgaca gaaacagtgt aggcattatg tattttcatg tagagtagga cccaaaaatc 2160
 caccxaaagt cttttatcta tgccacatcc ttcttatcta tacttccagg acactttttc 2220
 45 ttccttatga taaggctctc tctctctcca cacacacaca cacacacaca cacacacaca 2280
 cacacacaca cacaacaca cccccgcc accaagggtgc atgtaaaaag atgtagattc 2340
 ctctgccttt ctcatctaca cagcccagga gggtaagtta atataagagg gatttattgg 2400
 50 taagagatga tgcttaatct gttaacact gggcctcaaa gagagaattt cttttcttct 2460
 gtacttatta agcacctatt atgtgttgag cttatatata caaagggtta ttatatgcta 2520
 55 atatagtaat agtaatgggtg gttggtacta tgtaattac cataaaaatt attatccttt 2580

taaaaataag ctaattatta ttggatcttt tttagtattc attttatgtt ttttatgttt 2640
 5 ttgatttttt aaaagacaat ctcacctgtt tacccaggct ggagtgcagt ggtgcaatca 2700
 tagcttttctg cagtcttgaa ctcttgggct caagcaatcc tcctgccttg gcctcccaaa 2760
 gtgttgggat acagtcatga gccactgcat ctggcctagg atccatttag attaaaatat 2820
 10 gcatttttaa ttttaaaata atatggctaa tttttacctt atgtaatgtg tatactggta 2880
 ataaatctag tttgtgcct aaagttaa aa gtctttcca ataagcttca tgtacgtgag 2940
 15 gggagacatt taaagtgaag cagacagcca ggtgtggtgg ctacgcctg taatcccagc 3000
 actctgggag gctgagggtg gtggatcgct tgagccctgg agttcaagac cagcctgagc 3060
 20 aacatggcaa aacctgttt ctataacaaa aattagccgg gcatgggtggc atgtgcctgt 3120
 ggtcccagct actagggggc tgaggcagga gaatctttgg agcccaggag gtcaaggctg 3180
 cactgagcag tgcttgcgcc actgcactcc agcctgggtg acaggaccag acctgcctc 3240
 25 aaaaaataa gaagaaaaat taaaaataaa tggaacaac tacaagagc tgttgccta 3300
 gatgagctac ttagttaggc tgatatcttg gtatttaact tttaaagtca gggctctgca 3360
 30 cctgcactac attattaaaa tatcaattct caatgtatat ccacacaaag actggtacgt 3420
 gaatgttcat agtaccttta ttacacaaac ccaaagtag agactatcca aatatccatc 3480
 35 aacaagtga caaataaaca aaatgtgcta tatccatgca atggaatacc acctgcagt 3540
 acaaaggaag aagctacttg gggatgaatc ccaaagtcac gacgctaaat gaaagagtca 3600
 gacatgaagg aggagataat gtatgccata cgaaattcta gaaaatgaaa gtaacttata 3660
 40 gttacagaaa gcaaatcagg gcaggcatag aggctcacac ctgtaatccc agcactttga 3720
 gaggccacgt gggaagattg ctagaactca ggagtccaag accagcctgg gcaacacagt 3780
 45 gaaactccat tctccacaaa aatgggaaaa aaagaaagca aatcagtggg tgtcctgtgg 3840
 ggaggggaag gactgcaaag agggaagaag ctctggtggg gtgaggggtg tgattcaggt 3900
 50 tctgtatcct gactgtggtg gcagtttggg gtgtttacat ccaaaaatat tcgtagaatt 3960
 atgcatctta aatgggtgga gtttactgta tgtaaattat acctcaatgt aagaaaaaat 4020
 aatgtgtaag aaaagtttca attctcttgc cagcaaacgt tattcaaatt cctgagccct 4080
 55 ttacttcgca aattctctgc acttctgccc cgtaccatta ggtgacagca ctagctccac 4140

aaattggata aatgcatttc tggaaaagac tagggacaaa atccaggcat cacttgtgct 4200
 5 ttcatatcaa ccacgtgtga cagcttgtgt tgctgtctgc agctgcaatg gggactcttg 4260
 atttctttaa ggaaacttgg gtiaccagag tatttccaca aatgctattc aaattagtgc 4320
 ttatgatatg caagacactg tgctaggagc cagaaaacaa agaggaggag aaatcagtca 4380
 10 ttatgtggga acaacatagc aagatattta gatcattttg actagttaaa aaagcagcag 4440
 agtacaaaat cacacatgca atcagtataa tccaaatcat gtaaataatgt gcctgtagaa 4500
 15 agactagagg aataaacaca agaattctaa cagtcattgt cattagacac taagtctaata 4560
 tattattatt agacactatg atatttgaga tttaaaaaat ctttaatat ttaaaattta 4620
 gagctcttct atttttccat agtattcaag tttgacaatg atcaagtatt actctttctt 4680
 20 tttttttttt tttttttttt tttgagatgg agttttggtc ttgttgccca tgctggagtg 4740
 gaatggcatg accatagctc actgcaacct ccacctcctg ggttcaagca aagctgtcgc 4800
 25 ctcagcctcc cgggtagatg ggattacagg cggccaccac cacactcggc taatgtttgt 4860
 attttttagta gagatggggg ttcaccatgt tggccaggct ggtctcaaac tcctgacctc 4920
 30 agaggatcca cctgcctcag cctcccaaag tgctgggatt acagatgtag gccactgcgc 4980
 ccggccaagt attgctctta tacattaaaa aacaggtgtg agccactgcg cccagccagg 5040
 tatgtctctt atacattaaa aaataggcog gtgcagtggc tcacgcctgt aatcccagca 5100
 35 ctttgggaag ccaaggcggg cagaacaccc gaggtcagga gtccaaggcc agcctggcca 5160
 agatggtgaa accccgtctc tattaataat acaaacatta cctgggcatg atggtgggag 5220
 40 cctgtaatcc cagctactca ggaggtgag gcaggaggat ccgcgagacc tggcagatct 5280
 gcctgagcct gggaggttga ggctacagta agccaagatc atgccagtat acttcagcct 5340
 gggcgacaaa gtgagaccgt aacaaaaaaa aaaaaattta aaaaaagaaa tttagatcaa 5400
 45 gatccaactg taaaaagtgg cctaaacacc acattaaaga gtttgaggtt tattctgcag 5460
 gcagaagaga accatcaggg ggtcttcagc atgggaatgg catggtgcac ctggtttttg 5520
 50 tgagatcatg gtggtgacag tgtggggaat gttattttgg agggactgga ggcagacaga 5580
 ccggttaaaa ggccagcaca acagataagg aggaagaaga tgagggttg gaccgaagca 5640
 55 gagaagagca aacaggaag gtacaaattc aagaaatatt ggggggtttg aatcaacaca 5700

tttagatgat taattaaata tgaggactga ggaataagaa atgagtcaag gatggttcca 5760
 5 ggctgctagg ctgcttacct gaggtggcaa agtcgggagg agtggcagtt taggacaggg 5820
 ggcagttgag gaataattgtt ttgatcattt tgagtttgag gtacaagttg gacacttagg 5880
 taaagactgg aggggaaatc tgaatataca attatgggac tgaggaacaa gtttatttta 5940
 10 ttttttgttt cgttttcttg ttgaagaaca aatttaattg taatcccaag tcatcagcat 6000
 ctagaagaca gtggcaggag gtgactgtct tgtgggtaag ggtttggggt ccttgatgag 6060
 15 tatctctcaa ttggccttaa atataagcag gaaaaggagt ttatgatgga ttccaggctc 6120
 agcagggctc aggagggctc aggcagccag cagaggaagt cagagcatct tctttggttt 6180
 20 agcccaagta atgacttcct taaaaagctg aaggaaaatc cagagtgacc agattataaa 6240
 ctgtactctt gcattttctc tccctcctct caccacagc ctcttgatga accggaggaa 6300
 gtttctttac caattcaaaa atgtccgtg ggctaagggt cggcgtgaga cctacctgtg 6360
 25 ctacgtagtg aagaggcgtg acagtgtac atccttttca ctggactttg gttatcttcg 6420
 caataaggta tcaattaaag tcagctttgc aagcagtta atggtcaact gtgagtgtt 6480
 30 ttagagccac ctgctgatgg tattacttcc atcctttttt ggcatttgtg tctctatcac 6540
 attctcaaa tctttttttt tatttctttt tccatgtcca tgcaccata ttagacatgg 6600
 cccaaaatat gtgatttaat tcttcccag taatgtctggg caccctaata ccactcctc 6660
 35 cttcagtgcc aagaacaact gctcccaaac tgtttaccag ctttcctcag catctgaatt 6720
 gcctttgaga ttaattaagc taaaagcatt tttatatggg agaataattat cagcttgtcc 6780
 40 aagcaaaaat tttaaatgtg aaaaacaaat tgtgtcttaa gcatttttga aaattaagga 6840
 agaagaattt gggaaaaaat taacggtggt tcaattctgt tttccaaatg atttctttc 6900
 45 cctcctactc acatgggtcg taggccagtg aatacattca acatggtgat cccagaaaa 6960
 ctcagagaag ctcggctga tgattaatta aattgatctt tcggctaccc gagagaatta 7020
 catttccaag agacttcttc accaaaatcc agatggggtt acataaactt ctgcccattg 7080
 50 gtatctctc tctcctaaca cgctgtgacg tctgggcttg gtggaatctc agggaagcat 7140
 ccgtggggtg gaaggctcgc gtctggctcg ttgtttgatg gttatattac catgcaattt 7200
 55 tctttgccta cattgtatt gaatacatcc caatctcctt cctattcggg gacatgacac 7260

attctatttc agaaggcttt gatattatca agcactttca tttacttctc atggcagtg 7320
 5 ctattacttc tcttacaata cccatctgtc tgctttacca aaatctattt ccccttttca 7380
 gatcctccca aatggtcctc ataaactgtc ctgcctccac ctagtggtcc aggtatattt 7440
 ccacaatgtt acatcaacag gcacttctag ccattttcct tctcaaaagg tgcaaaaagc 7500
 10 aacttcataa acacaaatta aatcttcggt gaggtagtgt gatgctgctt cctcccaact 7560
 cagcgcactt cgtcttctc attccacaaa aacctatagc cttccttcac tctgcaggac 7620
 15 tagtgctgcc aagggttcag ctctacctac tgggtgtgctc ttttgagcaa gttgcttagc 7680
 ctctctgtaa cacaaggaca atagctgcaa gcatcccaa agatcattgc aggagacaat 7740
 20 gactaaggct accagagccg caataaaagt cagtgaattt tagcgtggc ctctctgtct 7800
 ctccagaacg gctgccacgt ggaattgtc ttcctccgct acatctcgga ctgggaccta 7860
 gaccctggcc gctgctaccg cgtcacctgg ttcacctct ggagcccctg ctacgactgt 7920
 25 gcccgacatg tggccgactt tctgcgaggg aacccaacc tcagtctgag gatcttcacc 7980
 gcgcgcctct acttctgtga ggaccgcaag gctgagcccg aggggctgcg gcggctgcac 8040
 30 cgcgccgggg tgcaaatagc catcatgacc ttcaaagggtg cgaaagggcc ttccgcgcag 8100
 gcgcagtgca gcagcccgca ttcgggattg cgatgcggaa tgaatgagtt agtggggaag 8160
 ctcgagggga agaagtgggc ggggattctg gttcacctct ggagccgaaa ttaaagatta 8220
 35 gaagcagaga aaagagtga tggctcagag acaaggcccc gaggaatga gaaaatggg 8280
 ccagggttgc ttctttcccc tcgatttga acctgaactg tcttctaccc ccatacccc 8340
 40 gccttttttt ctttttttt tttttgaag attattttta ctgctggaat actttttag 8400
 aaaaccacga aagaactttc aaagcctggg aagggtgca tgaaaattca gttcgtctct 8460
 ccagacagct tcggcgcatc cttttggtta ggggcttct cgtttttta attttcttc 8520
 45 tttctctaca gtctttttg gagtttcgta ttttcttat attttcttat tgttcaatca 8580
 ctctcagttt tcctctgatg aaaactttat ttctctcca catcagctt tcttctgct 8640
 50 gtttcacat tcagagccct ctgctaaggt tcctttccc tccctttct tcttttgtt 8700
 gtttcacatc tttaaatttc tgtctctccc cagggttgcg ttcttctct ggtcagaatt 8760
 55 cttttctct ttttttttt ttttttttt ttttttaaac aaacaaacaa aaaacccaaa 8820

aaaactcttt cccaatttac tttcttccaa catgttacaa agccatccac tcagtttaga 8880
 5 agactctccg gccccaccga cccccaacct cgttttgaag ccattcactc aatttgcttc 8940
 tctctttctc tacagccctt gtatgaggtt gatgacttac gagacgcatt tcgtactttg 9000
 ggactttgat agcaacttcc aggaatgtca cacacgatga aatatctctg ctgaagacag 9060
 10 tggataaaaa acagtccttc aagtcttctc tgtttttatt cttcaactct cactttctta 9120
 gagtttacag aaaaaatatt tatatacgac tctttaaaaa gatctatgtc ttgaaaatag 9180
 15 agaaggaaca caggtctggc cagggacgtg ctgcaattgg tgcagttttg aatgcaacat 9240
 tgccccctac tgggaataac agaactgcag gacctgggag catcctaaag tgtcaacgtt 9300
 20 ttctatgac ttttaggtag gatgagagca gaaggtagat cctaaaaagc atggtgagag 9360
 gatcaaagt ttttatatca acatccttta ttatttgatt catttgagtt aacagtgggtg 9420
 ttagtgatag atttttctat tcttttccct tgacgtttac tttcaagtaa cacaactct 9480
 25 tccatcaggc catgatctat aggacctcct aatgagagta tctgggtgat tgtgacccca 9540
 aaccatctct ccaaagcatt aatatccaat catgcgctgt atgttttaac cagcagaagc 9600
 30 atgtttttat gttgtacaa aagaagattg ttatgggtgg ggatggaggt atagaccatg 9660
 catggtcacc ttcaagctac ttttaataaag gatcttaaaa tgggcaggag gactgtgaac 9720
 aagacaccct aataatgggt tgatgtctga agtagcaaat cttctggaaa cgcaaactct 9780
 35 ttttaggaag tcctaattt agaaacaccc acaaacttca catatcataa ttagcaaaca 9840
 attggaagga agttgcttga atgttgggga gaggaatac tattggctct cgtgggtctc 9900
 40 ttcatctcag aaatgccaat caggtcaagg tttgctacat ttgtatgtg tgtgatgctt 9960
 ctcccaaagg tatattaact atataagaga gttgtgacaa aacagaatga taaagctgcg 10020
 45 aaccgtggca cacgtcata gttctagctg cttgggaggt tgaggaggga ggatggcttg 10080
 aacacaggtg ttcaaggcca gcctgggcaa cataacaaga tcctgtctct caaaaaaaaa 10140
 aaaaaaaaaa agaaagagag agggccgggc gtggtggctc acgcctgtaa tcccagcaact 10200
 50 ttgggaggcc gagccgggag gatcacctgt ggtcaggagt ttgagaccag cctggccaac 10260
 atggcaaac cccgtctgta ctcaaatgc aaaaattagc caggcgtggt agcaggcacc 10320
 55 tgtaatccca gctacttggg aggctgaggc aggagaatcg cttgaaccca ggaggtggag 10380

gttgcagtaa gctgagatcg tgccgttgca ctccagcctg ggcgacaaga gcaagactct 10440
 5 gtctcagaaa aaaaaaaaaa aaagagagag agagagaaaag agaacaatat ttgggagaga 10500
 aggatgggga agcattgcaa ggaaattgtg ctttatccaa casaatgtaa ggagccaata 10560
 10 agggatccct atttgtctct tttgggtgtc atttgtccct aacaactgtc tttgacagt 10620
 agaaaaatat tcagaataac catatccctg tgccgttatt acctagcaac ccttgcaatg 10680
 aagatgagca gatccacagg aaaacttgaa tgcacaactg tcttatttta atcttattgt 10740
 15 acataagttt gtaaaagagt taaaattgt tacttcatgt attcatttat attttatatt 10800
 attttgcgtc taatgatttt ttattaacat gatttccttt tctgatatat tgaaatggag 10860
 20 tctcaaagct tcataaattt ataactttag aatgattct aataacaacg tatgtaattg 10920
 taacattgca gtaatgggtc tacgaagcca tttctcttga tttttagtaa acctttatga 10980
 25 cagcaaattt gcttctggct cactttcaat cagttaaata aatgataaat aattttggaa 11040
 gctgtgaaga taaaatacca aataaaataa tataaaagt atttatatga agttaaata 11100
 aaaaatcagt atgatggaat aaacttgaga gtccagaagt tatcccatac atctgtaatc 11160
 30 aactaatttc tcacaagggt gtaaggacca ttcaatggag aaaa 11204

35 Claims

1. A DNA or a fragment thereof encoding a protein comprising the amino acid sequence of SEQ ID NO: 2 or 8.

2. The DNA or the fragment of claim 1, wherein the protein has a cytidine deaminase activity.

3. A DNA or a fragment thereof comprising the nucleotide sequence of SEQ ID NO: 1 or 7.

4. A DNA or a fragment thereof comprising a nucleotide sequence of (a) or (b) below:

(a) a nucleotide sequence comprising the nucleotide residues 93 to 689 of SEQ ID NO: 1 or

(b) a nucleotide sequence comprising the nucleotide residues 80 to 676 of SEQ ID NO: 7.

5. A DNA or a fragment of (a) or (b) below:

(a) a DNA or a fragment thereof that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1 and that encodes a mammal-derived protein being homologous to a protein that comprises the amino acid sequence of SEQ ID NO: 2 and having a cytidine deaminase activity or

(b) a DNA or a fragment thereof that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7 and that encodes a mammal-derived protein being homologous to a protein that comprises the amino acid sequence of SEQ ID NO: 8 and having a cytidine deaminase activity.

6. A protein or a fragment thereof comprising the amino acid sequence of SEQ ID NO: 2 or 8.

7. A protein or a fragment thereof comprising substantially the same amino acid sequence as that of SEQ ID NO: 2 or 8 and having a cytidine deaminase activity.

8. A protein of (a) or (b) below:

- (a) a mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 1, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 2, and that has a cytidine deaminase activity or
- (b) a mammal-derived protein that comprises an amino acid sequence encoded by a DNA hybridizing under stringent conditions with a DNA comprising the nucleotide sequence of SEQ ID NO: 7, that is homologous to a protein comprising the amino acid sequence of SEQ ID NO: 8, and that has a cytidine deaminase activity.

9. An expression vector comprising the DNA or the fragment of any one of claims 1 to 5.

10. A transformant transformed with the expression vector of claim 9.

11. An antibody or a portion thereof reactive to the protein of any one of claims 6 to 8 or to a fragment of the protein.

12. The antibody or the portion of claim 11, wherein the antibody is a monoclonal antibody.

13. A pharmaceutical composition comprising the antibody or the portion of claim 11 or 12, and a pharmaceutically acceptable carrier.

14. A cell producing a monoclonal antibody reactive to the protein of any one of claims 6 to 8 or to a fragment of the protein.

15. The cell of claim 14, wherein the cell is a hybridoma obtained by fusing, with a mammal-derived myeloma cell, a non-human mammal-derived B cell that produces a monoclonal antibody.

16. The cell of claim 15, wherein the cell is a transgenic cell transformed by introducing, into a cell, either or both of a DNA encoding a heavy chain of the monoclonal antibody and a DNA encoding a light chain of the monoclonal antibody.

17. A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (c) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10, or
- (c) SEQ ID NO: 35.

18. A genomic DNA or a fragment thereof comprising a nucleotide sequence of any one of (a) to (e) below:

- (a) SEQ ID NO: 11,
- (b) SEQ ID NO: 12,
- (c) SEQ ID NO: 13,
- (d) SEQ ID NO: 14, or
- (e) SEQ ID NO: 15.

19. A DNA comprising a complementary nucleotide sequence to an arbitrary partial nucleotide sequence of a nucleotide sequence of any one of (a) to (h) below:

- (a) SEQ ID NO: 9,
- (b) SEQ ID NO: 10,
- (c) SEQ ID NO: 11,
- (d) SEQ ID NO: 12,
- (e) SEQ ID NO: 13,
- (f) SEQ ID NO: 14,
- (g) SEQ ID NO: 15, or
- (h) SEQ ID NO: 35.

20. The DNA of claim 19, wherein the DNA comprises a nucleotide sequence of any one of (a) to (q) below:

- (a) SEQ ID NO: 18,
- (b) SEQ ID NO: 19,
- (c) SEQ ID NO: 20,
- (d) SEQ ID NO: 21,
- (e) SEQ ID NO: 22,
- (f) SEQ ID NO: 23,
- (g) SEQ ID NO: 24,
- (h) SEQ ID NO: 25,
- (i) SEQ ID NO: 26,
- (j) SEQ ID NO: 27,
- (k) SEQ ID NO: 28,
- (l) SEQ ID NO: 29,
- (m) SEQ ID NO: 30,
- (n) SEQ ID NO: 31,
- (o) SEQ ID NO: 32,
- (p) SEQ ID NO: 33, or
- (q) SEQ ID NO: 34.

21. Use of the DNA of claim 19 or 20 as a primer DNA in polymerase chain reaction.

22. Use of a pair of DNA of any one of (a) to (n) below as primer DNAs in polymerase chain reaction:

- (a) a DNA comprising the nucleotide sequence of SEQ ID NO: 31 and a DNA comprising the nucleotide sequence of SEQ ID NO: 32,
- (b) a DNA comprising the nucleotide sequence of SEQ ID NO: 20 and a DNA comprising the nucleotide sequence of SEQ ID NO: 22,
- (c) a DNA comprising the nucleotide sequence of SEQ ID NO: 21 and a DNA comprising the nucleotide sequence of SEQ ID NO: 30,
- (d) a DNA comprising the nucleotide sequence of SEQ ID NO: 24 and a DNA comprising the nucleotide sequence of SEQ ID NO: 25,
- (e) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (f) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (g) a DNA comprising the nucleotide sequence of SEQ ID NO: 23 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (h) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 27,
- (i) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (j) a DNA comprising the nucleotide sequence of SEQ ID NO: 26 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (k) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 28,
- (l) a DNA comprising the nucleotide sequence of SEQ ID NO: 34 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29,
- (m) a DNA comprising the nucleotide sequence of SEQ ID NO: 33 and a DNA comprising the nucleotide sequence of SEQ ID NO: 29, or
- (n) a DNA comprising the nucleotide sequence of SEQ ID NO: 18 and a DNA comprising the nucleotide sequence of SEQ ID NO: 19.

23. A method for identifying a substance that regulates transcription of a gene encoding an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8 into mRNA, or production of the AID protein, the method comprising the steps of:

- (a) culturing, separately in the presence and the absence of the substance, cells producing the AID protein and

(b) (i) comparing the level of the AID protein produced by the cells cultured in the presence of the substance with the level of the AID protein produced by the cells cultured in the absence of the substance or

(ii) comparing the level of the AID protein-encoding mRNA transcribed in the cells cultured in the presence of the substance with the level of the AID protein-encoding mRNA transcribed in the cells cultured in the absence of the substance.

24. A method for identifying a substance that regulates transcription of a gene encoding an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8 into mRNA, or production of the AID protein, the method comprising the steps of:

(a) culturing, separately in the presence and the absence of the substance, cells producing the AID protein and a protein other than the AID protein, wherein transcription of a gene encoding the other protein into mRNA is dependent in the cells on the degree of a signal of transcription of the gene encoding the AID protein into mRNA and

(b) comparing the level of the other protein produced by the cells cultured in the presence of the substance with the level of the other protein produced by the cells cultured in the absence of the substance.

25. The method of claim 23 or 24, wherein the cells are transgenic cells transformed with a gene encoding the protein.

26. The method of claim 24, wherein the cells are transgenic cells transformed with a gene encoding the protein and a gene encoding the other protein.

27. The method of claim 26, wherein the protein is a reporter protein.

28. The method of claim 27, wherein comparison of the level of the other protein is comparison of the level of a signal generated by the reporter protein.

29. The method of claim 27 or 28, wherein the reporter protein is luciferase.

30. A method for identifying a substance that inhibits an enzyme activity of an AID protein comprising the amino acid sequence of SEQ ID NO: 2 or 8, the method comprising the step of (a) or (b) below:

(a) culturing, separately in the presence and the absence of the substance, mammal-derived B cells or tissues comprising the B cells, and comparing enzyme activities of the AID proteins in the B cells separately cultured or

(b) (i) administering the substance separately to an AID gene knockout mouse whose endogenous AID gene is inactivated so that transcription of the endogenous AID gene into mRNA is inhibited, and to a normal mouse and

(ii) comparing enzyme activities of the AID proteins in the B cells isolated from the respective mice.

31. The method of claim 30, wherein the enzyme activity is a cytidine deaminase activity.

Figure 1

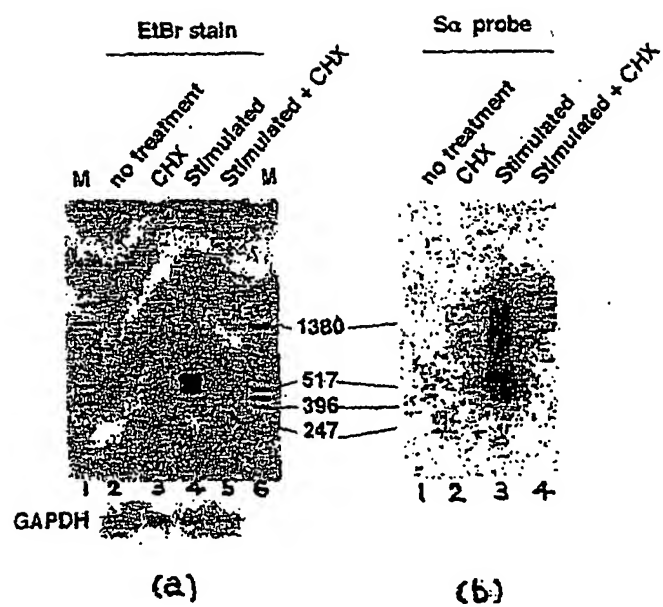


Figure 2

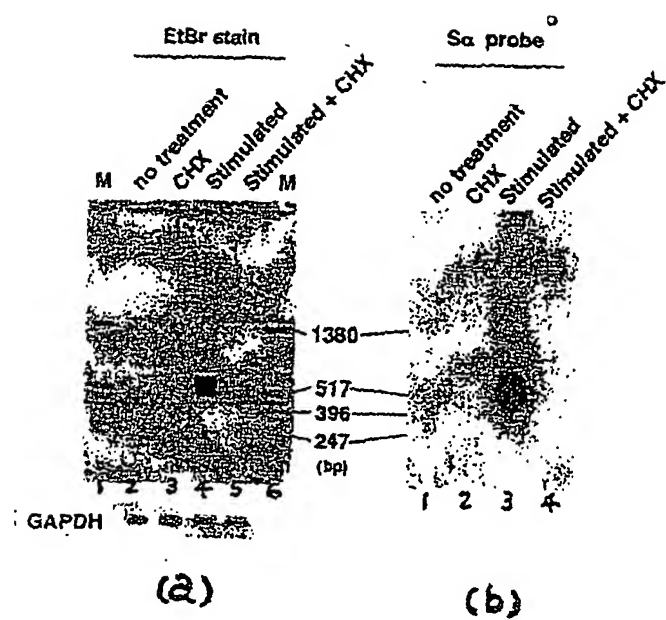


Figure 3

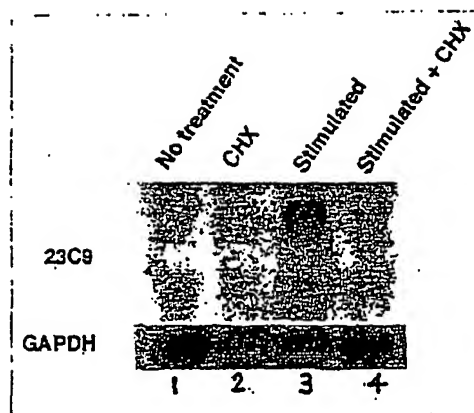


Figure 4

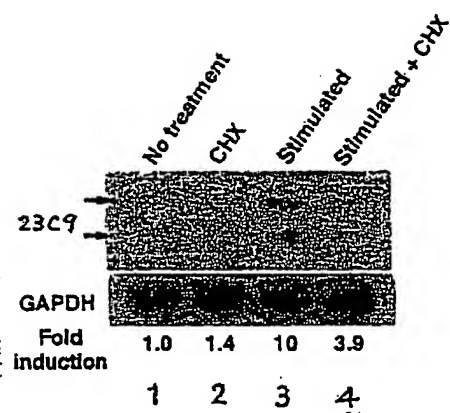


Figure 5

mAID	1	M--D--SL-L-MK-QKF-LYHFKNVRW-AGK- Q HETTYLCYVVKRRDSATSCS L DFG L LR	50
mAPOBEC-1	1	MSSETGPVAVDPTLRRRIEPHEF-EVFFDPREL R KETC L LYEIN-W-GGRH-SV-WR I TS	55
mAID	51	NKSGCHIV L ELL L FL-RYISDWDLP-GRCYRV I WFTSWSPCYOCARHV A EFLRWNPVLS L RI	108
mAPOBEC-1	56	QNTSNIV E VNF L EKF T TERYFRPN T RC-SII I WFLSWSPCGECSRA I TEFLSRHPYV T LFI	114
mAID	109	FTARLYFCE D RKAEP E GLR R LHRAGV Q IGIM T FKDYFYC H NTFVENR R TFK A MEGL H EN	168
mAPOBEC-1	115	YIARLYHHTD Q R-NR Q GLR L LISSGV T IQIM T EQEYCYCWR N FVNYP P SNEAY P RYPH L	173
mAID	169	SVRL-TR Q LRRL L PL E -VDDLRDAFR M L G F-----	198
mAPOBEC-1	174	WVKLYVLE L YCH I LG L PPCLK I LR R K Q P Q L T FTITLQ T CHY Q R I PP H LLW A T G L K	229

Figure 6

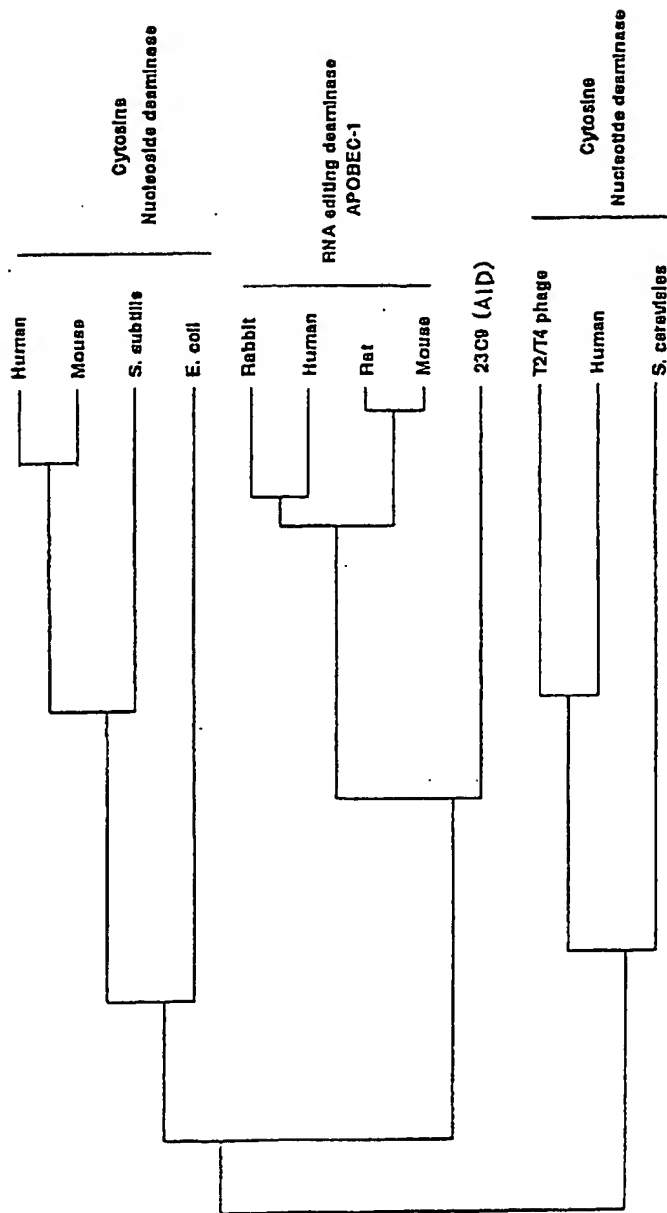


Figure 7

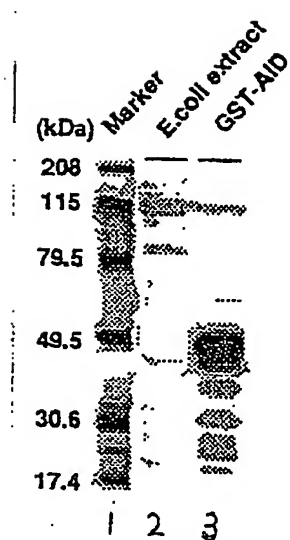


Figure 8

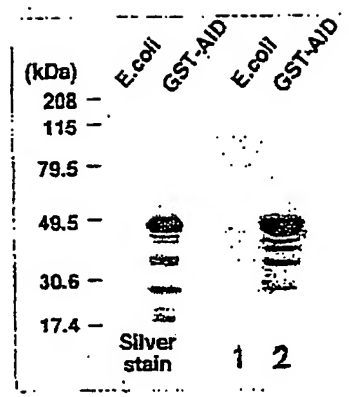


Figure 9

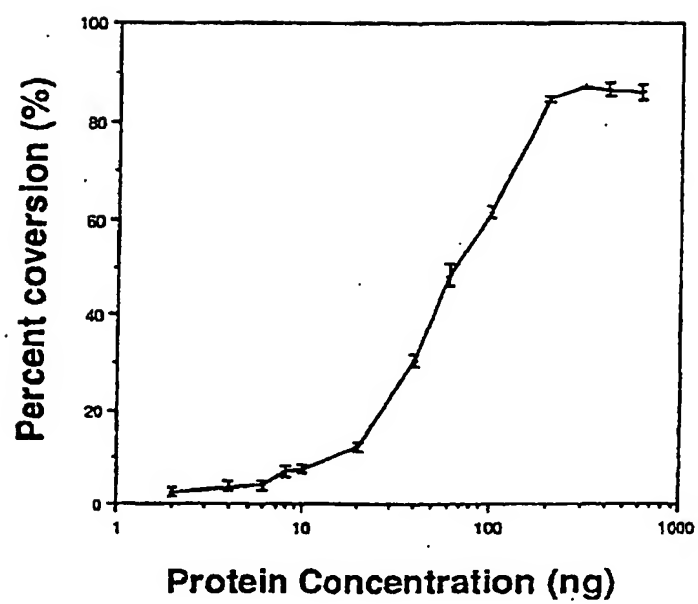


Figure 10

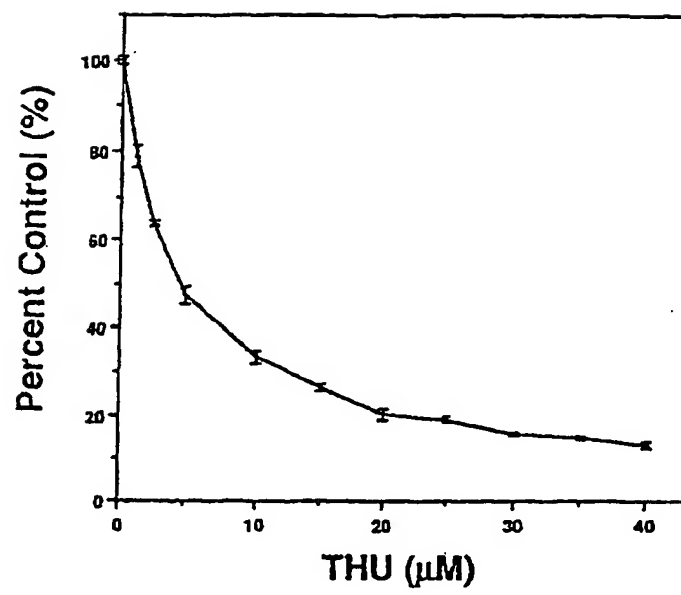


Figure 11

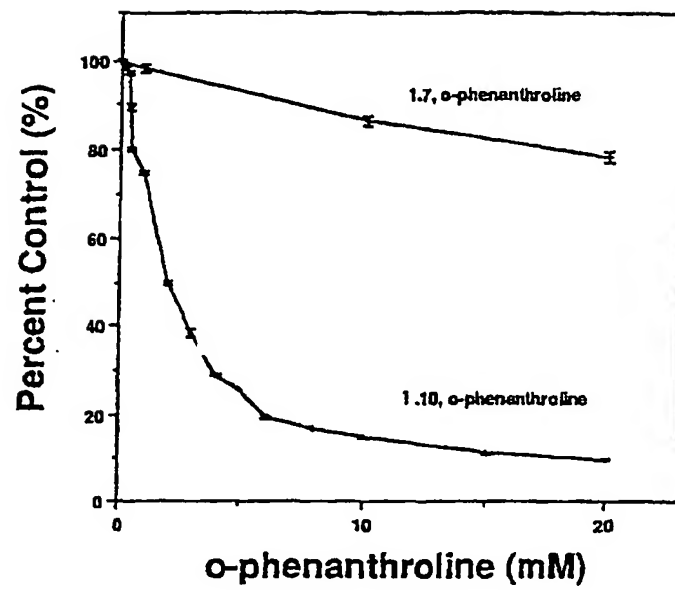


Figure 12

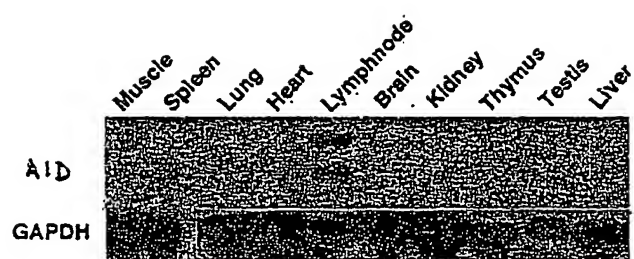


Figure 13

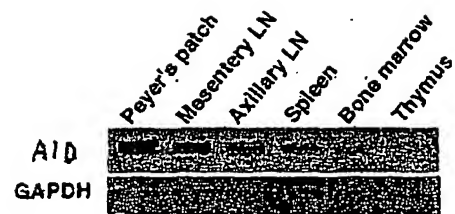


Figure 14

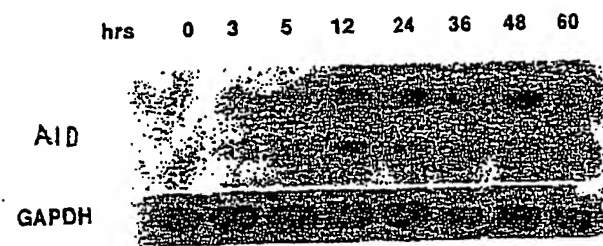


Figure 15

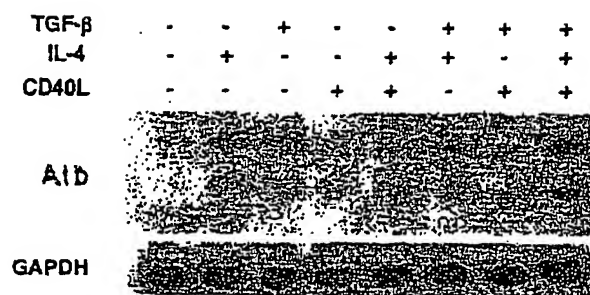


Figure 16

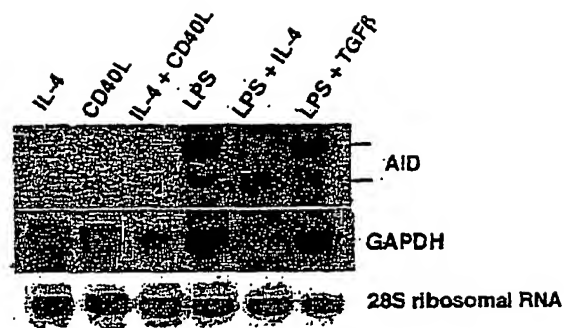


Figure 17

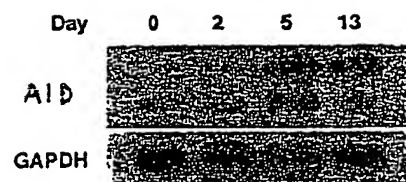


Figure 18

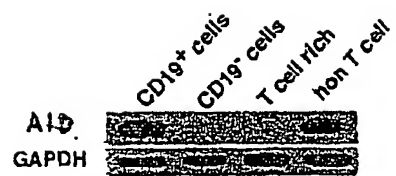


Figure 19

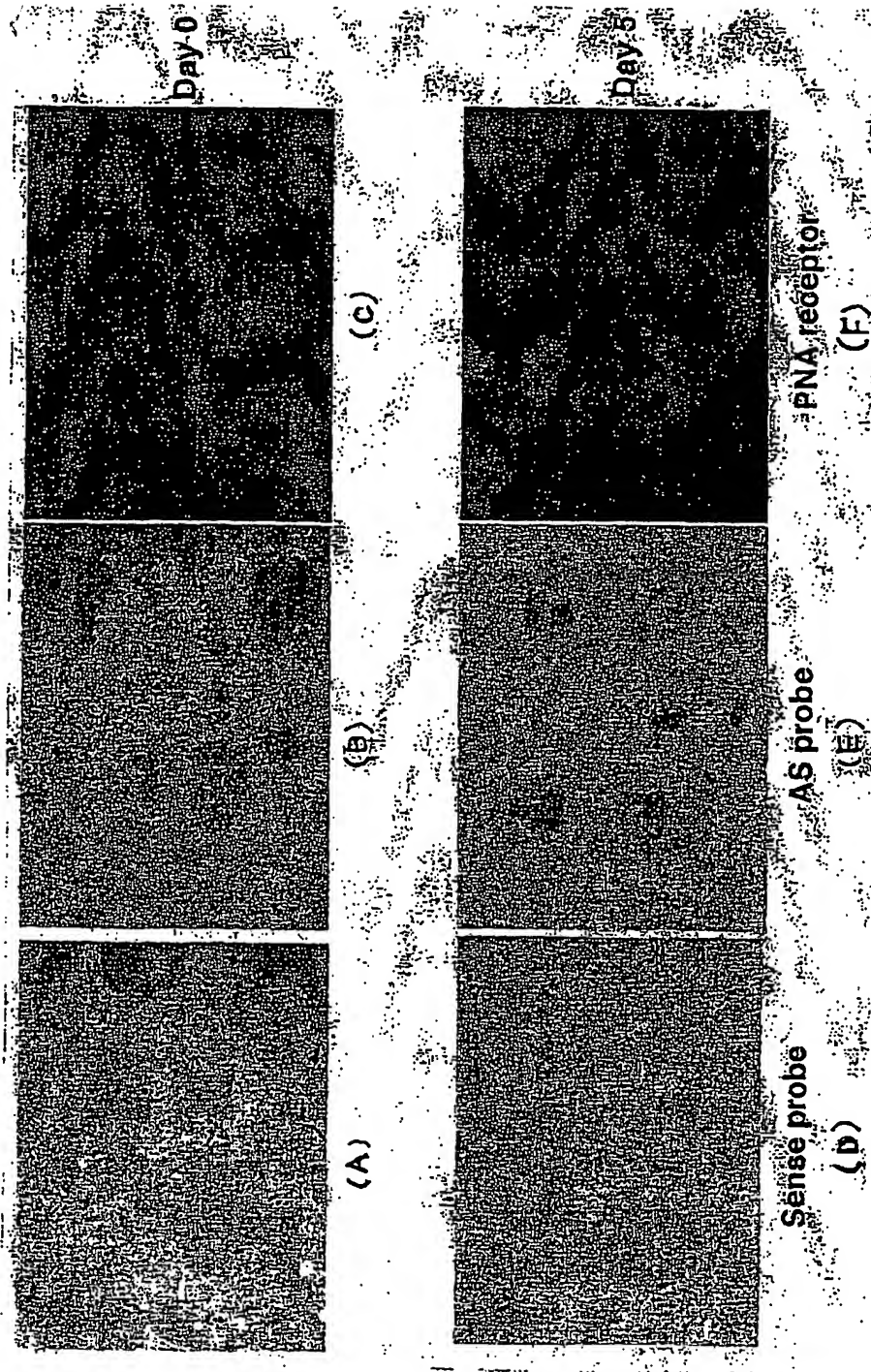


Figure 20

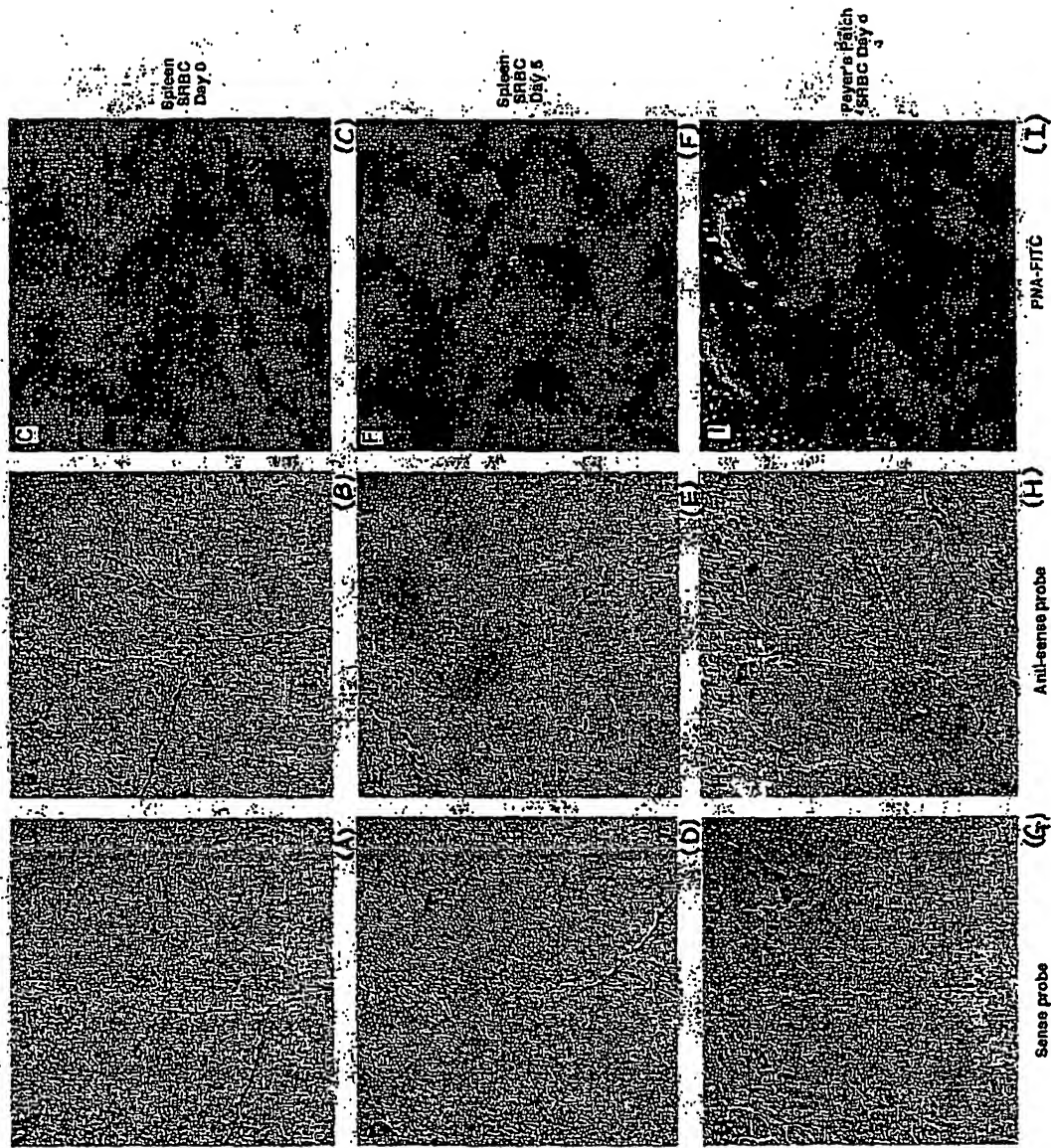


Figure 21

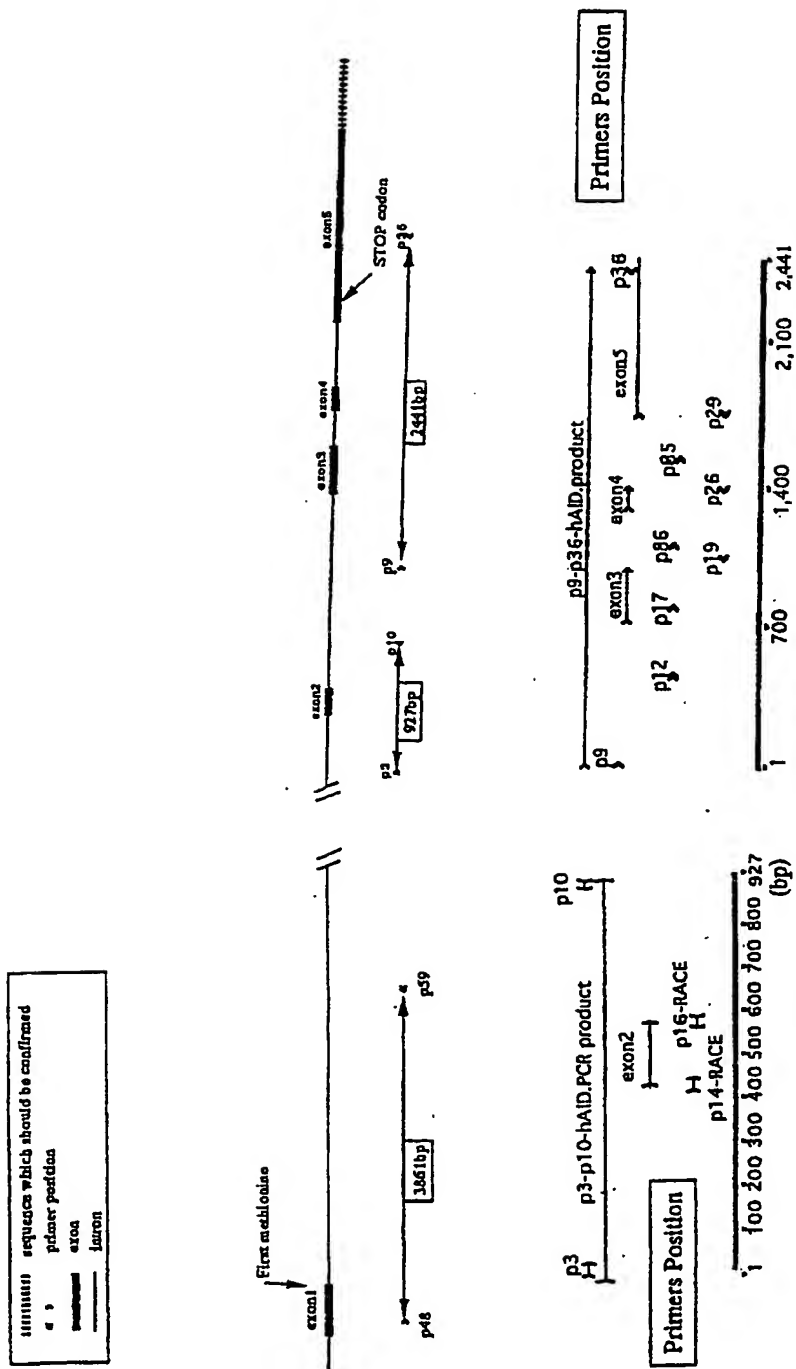


Figure 22

```

Human : 1  MDSLMMNRKFLYQFNVRWAKGRRETYLCYVVKRDSATSFSLDFGYLRNKGCHVELL 60
          ***** ++*****
Mouse : 1  MDSLMMKQKKFLYHFNVRWAKGRRETYLCYVVKRDSATSCSLDFGHLRNKSGCHVELL 60
          ***** ++*****

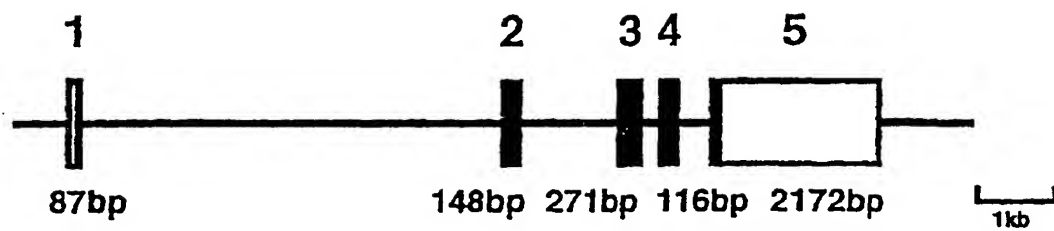
Human : 61  FLRYISDWDLDPGRCYRVTTWTTSWSPCYDCARVADFLRGNPNLSLRIFTARLYTCEDRK 120
          ***** ++*****
Mouse : 61  FLRYISDWDLDPGRCYRVTTWTTSWSPCYDCARVADFLRGNPNLSLRIFTARLYTCEDRK 120
          ***** ++*****

Human : 121 AEPEGLRRLHRAGVQIAINTFDYFYCWNTFVENHERTFKAWEGHENSVRLSRQLRRIL 180
          ***** ++*****
Mouse : 121 AEPEGLRRLHRAGVQIGINTFDYFYCWNTFVENRERTFKAWEGHENSVRLTRQLRRIL 180
          ***** ++*****

Human : 181 LPLYEVDDLRLDAFRTLGL 198
          ***** **
Mouse : 181 LPLYEVDDLRLDAFRMLGF 198
          ***** **

```

Figure 23



Exons	5' Splice Donor	3' Splice Acceptor	Exons
1	GACAGgt	agCCTCT	2
2	ATAAGgt	agAACGG	3
3	CAAAGgt	agATTAT	4
4	TTTGgt	agCCCT	5

Figure 24

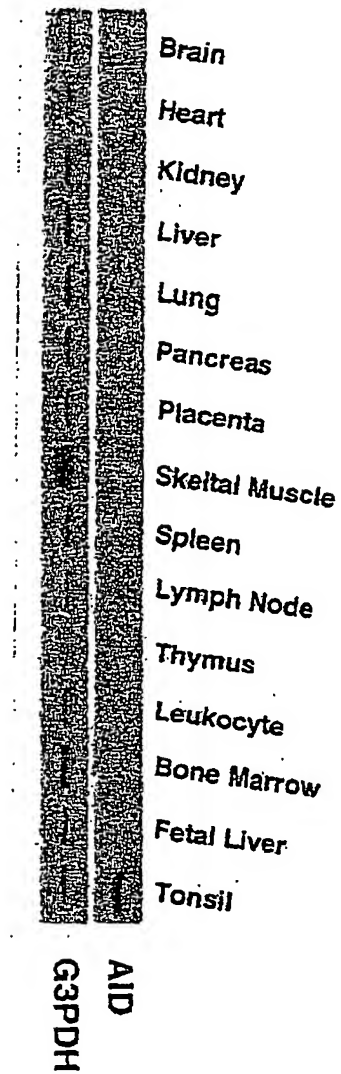
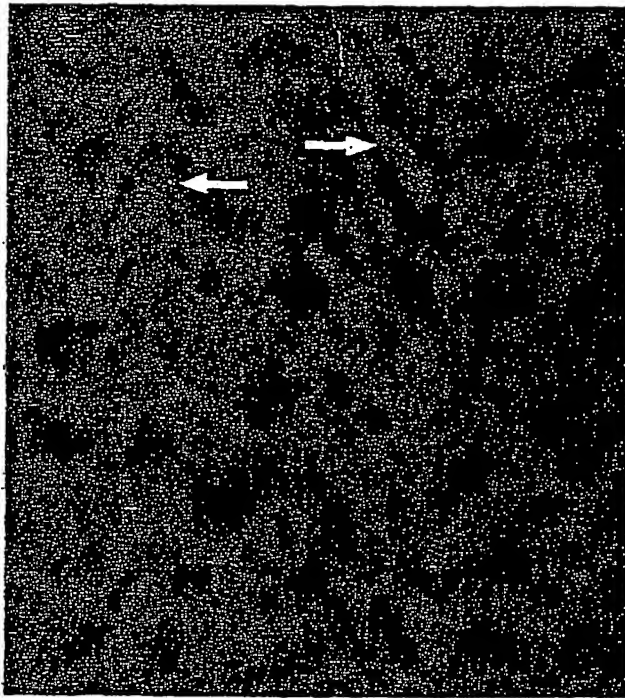


Figure 25



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/01918

A. CLASSIFICATION OF SUBJECT MATTER Int.Cl ⁷ C12N15/55, C12N5/10, C12P21/08, C07K16/40 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int.Cl ⁷ C12N15/55, C12N5/10, C12P21/08, C07K16/40 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPI, WPI/L, BIOSIS PREVIEWS, CAS ONLINE, GenBank/EMBL/DDBJ/GeneSeq		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	Muramatsu M. et al., "Specific Expression of Activation-induced Cytidine Deaminase (AID), a Novel Member of the RNA-editing Deaminase Family in Germinal Center B Cell" J. Biol. Chem., Vol. 274, No. 26 (June, 1999) p. 18470-18476	1-31
A	Anant S. et al., "apobec-1, the catalytic subunit of the mammalian apolipoprotein B mRNA editing enzyme, is a novel RNA-binding protein.", J Biol Chem. (1995), Vol. 270, No. 24, p. 14762-14767	1-31
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 20 June, 2000 (20.06.00)		Date of mailing of the international search report 18 July, 2000 (18.07.00)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)